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# SEARCH REQUEST FORM

Requestor's Name: \_\_\_\_\_ Serial Number: \_\_\_\_\_  
Date: \_\_\_\_\_ Phone: \_\_\_\_\_ Art Unit: \_\_\_\_\_

## Search Topic:

Please write a detailed statement of search topic. Describe specifically as possible the subject matter to be searched. Define any terms that may have a special meaning. Give examples or relevant citations, authors, keywords, etc., if known. For sequences, please attach a copy of the sequence. You may include a copy of the broadest and/or most relevant claim(s).

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## STAFF USE ONLY

Date completed: 08-20-02  
Searcher: Beverly C4994  
Terminal time: 20  
Elapsed time: \_\_\_\_\_  
CPU time: \_\_\_\_\_  
Total time: 25  
Number of Searches: \_\_\_\_\_  
Number of Databases: 1

### Search Site

\_\_\_\_ STIC  
\_\_\_\_ CM-1  
\_\_\_\_ Pre-S

### Type of Search

\_\_\_\_ N.A. Sequence  
\_\_\_\_ A.A. Sequence  
\_\_\_\_ Structure  
\_\_\_\_ Bibliographic

### Vendors

\_\_\_\_ IG  
\_\_\_\_ STN  
\_\_\_\_ Dialog  
\_\_\_\_ APS  
\_\_\_\_ Geninfo  
\_\_\_\_ SDC  
\_\_\_\_ DARC/Questel  
☒ Other CGN

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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 19, 2002, 19:24:00 ; Search time 1864.41 Seconds

(without alignments)  
8350.815 Million cell updates/sec

Title: US-09-898-554-13

Perfect score: 744  
Sequence: 1 atgaccttgcagcaagat.....caatcattgcacatttag 744

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

GenBank:  
1: gb\_da:\*  
2: gb\_hlg:\*  
3: gb\_in:\*  
4: gb\_cm:\*  
5: gb\_ov:\*  
6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_scs:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vl:\*  
15: em\_ba:\*  
16: em\_fun:\*  
17: em\_hum:\*  
18: em\_in:\*  
19: em\_mu:\*  
20: em\_om:\*  
21: em\_or:\*  
22: em\_ov:\*  
23: em\_ph:\*  
24: em\_pl:\*  
25: em\_ro:\*  
26: em\_ri:\*  
27: em\_sts:\*  
28: em\_un:\*  
29: em\_vl:\*  
30: em\_hlg\_hum:\*  
31: em\_hlg\_inv:\*  
32: em\_hlg\_other:\*  
33: em\_higo\_inv:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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1	668.2	89.8	3763	10	AF303744	AF303744 Mus muscu
2	526.8	70.8	3750	10	AB005900	AB005900 Rattus no
3	298.2	40.1	1318	6	AR077718	AR077718 Sequence
4	298.2	40.1	1318	6	AR138263	AR138263 Sequence
5	298.2	40.1	1318	6	E12916	E12916 Human CDNA
6	298.2	40.1	2067	9	AF035776	AF035776 Homo sapi
7	298.2	40.1	2463	9	AB010710	AB010710 Homo sapi
8	298.2	40.1	2480	9	BC022295	BC022295 Homo sapi
9	293.6	39.5	1578	4	AB018668	AB018668 Sus scrof
10	287.2	38.6	1879	4	D89049	D89049 Bos taurus
11	287.2	38.6	1897	6	AR077716	AR077716 Sequence
12	287.2	38.6	1897	6	E12914	E12914 Bovine CDNA
13	287.2	38.6	1897	6	E12914	E12914 Bovine CDNA
14	287.2	38.6	1906	6	AR138262	AR138262 Sequence
15	287.2	38.6	1906	6	E12915	E12915 Bovine CDNA
16	287.2	38.6	1906	6	AB016237	AB016237 Oryctolag
17	277.6	37.3	1514	4	AB018097	AB018097 Rattus no
18	127.8	17.2	278	10	AB018097	AB018097 Rattus no
19	125.4	16.9	162	10	AB018097	AB018097 Rattus no
20	114.4	15.4	161	10	AB018097	AB018097 Rattus no
21	108.4	14.6	169	10	AB018097	AB018097 Rattus no
22	106.2	14.3	162	10	AB018097	AB018097 Rattus no
23	103	13.8	240864	2	AC006510	AC006510 Homo sapi
24	102	13.7	260	9	AB017441	AB017441 Homo sapi
25	102	13.7	328	9	HS0183	HS0183 Homo sapi
26	102	13.7	15387	9	HS0183	HS0183 Homo sapi
27	102	13.7	182211	2	AC024224	AC024224 Homo sapi
28	90.6	12.2	140	10	AB018097	AB018097 Rattus no
29	74.4	10.0	534	6	E21012	E21012 Novel membr
30	74.4	10.0	741	6	E21012	E21012 Novel membr
31	74.4	10.0	744	9	AY026769	AY026769 Homo sapi
32	74.4	10.0	744	9	AF400595	AF400595 Homo sapi
33	74.4	10.0	1153	9	HS0183	HS0183 Homo sapi
34	74.4	10.0	1606	9	AF313468	AF313468 Homo sapi
35	74.4	10.0	2681	9	HS0183	HS0183 Homo sapi
36	74.4	10.0	240864	2	AC006510	AC006510 Homo sapi
37	73.4	9.9	154	9	AB017441	AB017441 Homo sapi
38	72.4	9.7	507	9	AF400599	AF400599 Homo sapi
39	72.4	9.7	603	6	E21011	E21011 Novel membr
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41	72.4	9.7	606	9	AF400596	AF400596 Homo sapi
42	72.4	9.7	990	6	AR035946	AR035946 Sequence
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44	72.4	9.7	1015	6	HS0183	HS0183 Homo sapi
45	72.4	9.7	2349	9	AF313469	AF313469 Homo sapi

## ALIGNMENTS

RESULT 1  
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LOCUS AF303744  
DEFINITION Mus musculus oxidized LDL receptor (lox-1) mRNA, complete cds.  
ACCESSION AF303744  
VERSION AF303744.1 GI:12006985  
KEYWORDS  
SOURCE house mouse.  
ORGANISM Mus musculus.

REFERENCE  
1 (bases 1 to 3763)  
Mammalia: Eutheria; Rodentia: Sciurognathi; Muridae; Murinae; Mus.  
AUTHORS Park,S.-H., Ahn,H.-J. and Cho,J.-J.  
TITLE Mouse LOX-1 is expressed in mast cells after Ige cross-linking  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 3763)  
Park,S.-H., Ahn,H.-J. and Cho,J.-J.  
AUTHORS Direct Submission  
TITLE Submitted (07-SEP-2000) Microbiology, Kyung Hee University, College of Medicine, Dongdaemun-Gu, Hoeki-Dong 1, Seoul, Korea  
JOURNAL Location/Qualifiers  
FEATURES  
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Best Local Similarity	98.8%; Pred. No. 3.5e-176;		
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Dd	459	AACCTTCAGAGAGATCCCGAGAGAAGCAAGGAATAATGACACCATCCCGGANG	518
Oy	124	ctgacgcgaaatcccaaagcaggaagagcttctgcagatgatcagaacctccaagaa	183
Dd	519	CTGGAGCGAAGAAATCCAAAAGCGAGAGAGAGCTTTGCAGATGATTGACAACCTCCAAGA	578
Oy	184	gcccgccagagagctgcgaaactcttcagagaggtcccagagagactcaagggaagata	243
Oy	579	GCCCTGCGAGAGAGCTGCAAAACTCTTCAGAGGAGTGCCCAAGAGAACTCAAAGGAAAA	638
Oy	244	gacaccctaaccttgaagcttgacagagaagaatccaaagcagagagagctttcacagaag	303
Dd	639	GACACCCTCACCTTAAGAGTGAAAGCAAGCAATCCAAAAGCAGAGAGAGCTTTACAGANG	698
Oy	304	aatcagaacctccaagaagccctgcgaagaagctgcgaactttcagtlcctgtccaca	363
Dd	699	AATCGAAGACCTTCAAGAAAGCCCTGCAAAAAGAGCTGCAAACTTTTCAGAGTCTTGTCACAA	758
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Dd	759	GACTGCTCTGGCATTAAGAAAAAAGCTTACCTTCCTTCAGAGGCCCTTTAGCTGGGAAAA	818
Oy	424	aaccgcagacctgcgaactcttgggtgagcagttactcaaatbaatatgtgacatatgat	483
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Oy	484	ctgacattcatcttaagaagaatttcccaataccacctccccattctgatttgattgeat	543
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Dd	939	CGGAAGAACCCCTGCGCAACCATGCGTATGGGAGAAATGGAATCTTTGAAATTTTCAATTC	998
Oy	604	ttaaagaccagagggcgttcttcttaacagctataattcaagaagaactgtgcataacctcaa	663
Dd	999	TTTAAGACCAAGGGCGCTTTCTTTACAGCTAATTTATCATCAGGCAAGCTGTGCATACCTTCAA	1058

Qy	664	gacggagcgtcttcgcggaacacgcattcattgcattcaagatatgtcagaagag	723
Db	1055	GACGGAGCTGCTTTCGCTGGAACATCTTAAATTCATTCAGCATATGTGAGAGAAG	1118
Qy	774	acaatcatttcgaatttag	744
Db	1119	ACAATCATTTGCAATTTAG	1139
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LOCUS	AB005900	3750 bp	linear
DEFINITION	Rattus norvegicus mRNA for endothelial receptor for oxidized low-density lipoprotein, complete cds.		
ACCESSION	AB005900		
VERSION	AB005900.1	GI:307773	
KEYWORDS	endothelial receptor for oxidized low-density lipoprotein.		
SOURCE	Rattus norvegicus (strain:SHR-SP) 13 weeks old male kidney cDNA to mRNA.		
ORGANISM	Rattus norvegicus		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.		
REFERENCE	1 (bases 1 to 3750)		
AUTHORS	Fujita,T.		
TITLE	Direct Submission		
JOURNAL	Submitted (19-JUL-1997) Toshiro Fujita, University of Tokyo School of Medicine, Fourth Department of Internal Medicine, 3-28-6 Mejirodai, Bunkyo-ku, Tokyo 112, Japan, Tokyo 112, Japan (E-mail:tfujita@ishn.u-tokyo.ac.jp, Tel:+81-3-3943-1151, Fax:+81-3-3942-5690)		
REFERENCE	2 (sites)		
AUTHORS	Nagase,M., Hirose,S. and Fujita,T.		
TITLE	Unique repetitive sequence and unexpected regulation of expression of rat endothelial receptor for oxidized low-density lipoprotein (LOX-1)		
JOURNAL	Biochem. J. 330 (Pt 3), 1417-1422 (1998)		
MEDLINE	98161826		
COMMENT	Sequence updated (11-Oct-1997).		
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	/note="ARE:A+U-rich element; motif for rapid degradation of mRNA"		
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OK protein - protein search, using sw model

Run on: August 19, 2002, 22:57:24 ; Search time 68.99 Seconds

(without alignments)  
619.361 Million cell updates/sec

Title: US-09-898-554-14

Perfect score: 1339

Sequence: 1 MTFDDKMKPANDPDKSCG.....ENCILIAFSICCKTKTNHLQI 247

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :  
1: SP\_ARCHAEA:  
2: SP\_BACTERIA:  
3: SP\_FUNGI:  
4: SP\_HUMAN:  
5: SP\_INVERTEBRATE:  
6: SP\_MAMMAL:  
7: SP\_MHC:  
8: SP\_ORGANELLE:  
9: SP\_PHAGE:  
10: SP\_PLANT:  
11: SP RODENT:  
12: SP\_VIRUS:  
13: SP\_VERTEBRATE:  
14: SP\_UNCLASSIFIED:  
15: SP\_VIRUS:  
16: SP\_BACTERIAP:  
17: SP\_ARCHAEP:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1241	94.1	363	11 O9EQ09	O9EQ09 mus musculus
2	972	73.7	364	11 O70156	O70156 rattus norv
3	643	48.7	278	6 O9XTRA8	O9XTRA8 oryctolagus
4	639	48.4	274	6 O9TWR7	O9TWR7 sus scrofa
5	637	48.3	273	4 P78380	P78380 homo sapien
6	596	45.2	270	6 P79391	P79391 bos taurus
7	258	19.6	247	4 O9BXN2	O9BXN2 homo sapien
8	251.5	19.1	168	4 O96PA7	O96PA7 homo sapien
9	251	19.0	201	4 O9H1K3	O9H1K3 homo sapien
10	231	17.5	244	11 O9J150	O9J150 mus musculus
11	224.5	17.0	381	6 O95LA8	O95LA8 macaca mela
12	223.5	16.9	381	6 O95LC6	O95LC6 macaca mela
13	223	16.9	360	4 O96Q04	O96Q04 homo sapien
14	223	16.9	380	4 O96Q05	O96Q05 homo sapien
15	223	16.9	380	4 O96Q00	O96Q00 homo sapien
16	223	16.9	404	4 O9NNX6	O9NNX6 homo sapien

17	223	16.9	404	4 O96Q01	O96Q01 homo sapien
18	222.5	16.9	404	6 O95J96	O95J96 macaca mela
19	221	16.8	280	4 O9NZH3	O9NZH3 homo sapien
20	219.5	16.6	223	11 O925G3	O925G3 mus musculus
21	218.5	16.6	217	11 O64228	O64228 mus sp. nki
22	216.5	16.4	275	11 O9D403	O9D403 mus musculus
23	212	16.1	268	4 O96Q03	O96Q03 homo sapien
24	212	16.1	404	6 O95I98	O95I98 pan troglod
25	211	16.0	334	4 O96Q09	O96Q09 homo sapien
26	210	15.9	334	4 O96Q08	O96Q08 homo sapien
27	206.5	15.7	227	11 O925G4	O925G4 mus musculus
28	205	15.5	312	4 O96Q07	O96Q07 mus musculus
29	204.5	15.5	223	11 O95JB4	O95JB4 mus musculus
30	204.5	15.5	223	11 O99P32	O99P32 mus musculus
31	203.5	15.4	295	11 O912M4	O912M4 mus musculus
32	203.5	15.4	311	11 O98SV4	O98SV4 mus musculus
33	203.5	15.4	325	11 O912X8	O912X8 mus musculus
34	202.5	15.4	227	11 O61973	O61973 mus musculus
35	201.5	15.3	227	11 O91V25	O91V25 mus musculus
36	200.5	15.2	223	11 O925G5	O925G5 mus musculus
37	195.5	14.8	224	11 O61970	O61970 mus musculus
38	192.5	14.6	189	11 O61969	O61969 mus musculus
39	192.5	14.6	263	4 O96Q03	O96Q03 homo sapien
40	191.5	14.5	229	11 O9JL99	O9JL99 mus musculus
41	191	14.5	332	4 O96Q05	O96Q05 homo sapien
42	190	14.4	309	11 O63097	O63097 rattus norv
43	189.5	14.4	198	11 O9DBL1	O9DBL1 mus musculus
44	187.5	14.2	156	13 O73894	O73894 gallus gall
45	186.5	14.1	230	11 O54871	O54871 rattus norv

## ALIGNMENTS

RESULT 1.  
ID O9EQ09 PRELIMINARY; PRT; 363 AA.  
AC O9EQ09;  
DT 01-MAR-2001 (TREMBLrel. 16, Created)  
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
DE OXIDIZED LDL RECEPTOR.  
GN LOX-1.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
OC NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Park S.-H., Ahn H.-J., Cho J.-J.;  
RT "Mouse LOX-1 is expressed in mast cells after Ige cross-linking."  
RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF303744; AAC4498.1; -  
DR InterPro; IPR001304; lectin.C.  
DR Pfam; PF00059; lectin.C; 1.  
DR SMART; SM00034; CLECT; 1.  
DR PROSITE; PSS0041; C\_TYPE\_LECTIN\_2; 1.  
KW Receptor.  
SQ SEQUENCE 363 AA; 41613 MW; E44703D6408F15F8 CRC64;

Query Match 94.1%; Score 1241; DB 11; Length 363;  
Best Local Similarity 67.5%; Pred. No. 4.6e-80;  
Matches 245; Conservative 0; Mismatches 2; Indels 116; Gaps 1;

OY 1 MTFDDKMKPANDPDKSCGKKR-----24  
DB 1 MTFDDKMKPANDPDKSCGKKRGLHLLSPWFPAAATLVILCVLSTLVQWOTLR 60  
OY 25 -----24  
DB 61 QVSDLLKQYQANLTQODRIIEGQWLAQQAENASQESKELKGIPTLTOKLNEKSEOE 120

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OY 25 -----ESORELKGIDITITRKLDEKSEKEOELLQONLOEALQ 64
DB 121 ELLQKNQNOEALQRAANSSESORELKIDITITRKLDEKSEKEOELLQONLOEALQ 180
OY 65 RAANSSESORELKIDITITRKLDEKSEKEOELLQONLOEALQRAANSFGPCQDWL 124
DB 181 RAANSSESORELKIDITITRKLDEKSEKEOELLQONLOEALQRAANSFGPCQDWL 240
OY 125 WKRENCYLFGHPGWEKNQOTCSLGGOLQINGADDLFTIIQAISSHTSPFWIGLHRRK 184
DB 241 WKRENCYLFGHPGWEKNQOTCSLGGOLQINGADDLFTIIQAISSHTSPFWIGLHRRK 300
OY 185 PGQPLWENGTPLNFOFFTRGVSLQIYSSNCAYIQDGAFAENCILIAFSICOKKTNH 244
DB 301 PGQPLWENGTPLNFOFFTRGVSLQIYSSNCAYIQDGAFAENCILIAFSICOKKTNH 360
OY 245 LQI 247
DB 361 LQI 363

RESULT 2
ID 070156 PRELIMINARY; PRT; 364 AA.
AC 070156:
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE ENDOThELIAL RECEPTOR FOR OXIDIZED LOW-DENSITY LIPOPROTEIN.
GN LOX-1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SHR.SP; TISSUE=KIDNEY;
RC MEDLINE=9811826; PubMed=9494115;
RA Nagase M., Hirose S., Fujita T.;
RT "Unique repetitive sequence and unexpected regulation of expression of
RT rat endothelial receptor for oxidized low-density lipoprotein (LOX-
RT 1).";
RL Biochem. J. 330:1447-1452(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=SPRAGUE-DAWLEY; TISSUE=LIVER;
RC MEDLINE=99057940; PubMed=9837956;
RA Nagase M., Abe J., Takahashi K., Ando J., Hirose S., Fujita T.;
RT "Genomic organization and regulation of expression of the lectin-like
RT oxidized low-density lipoprotein receptor (LOX-1) gene.";
RL J. Biol. Chem. 273:33702-33707(1998).
DR EMBL; AB005900; BAA25785.1; -
DR EMBL; AB018104; BAA35123.1; -
DR EMBL; AB018097; BAA35123.1; JOINED.
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DR EMBL; AB018100; BAA35123.1; JOINED.
DR EMBL; AB018101; BAA35123.1; JOINED.
DR EMBL; AB018102; BAA35123.1; JOINED.
DR EMBL; AB018103; BAA35123.1; JOINED.
DR InterPro: IPR001304; lectin_c.
DR Pfam: PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
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SQ SEQUENCE 364 AA; 41890 MW; 0AD2839C07206E09 CRC64;

Query Match 73.7%; Score 972; DB 11; Length 364;
Best Local Similarity 53.2%; Pred. No. 4.3e-61;
Matches 192; Conservative 23; Mismatches 30; Indels 116; Gaps 2;
1 MTFDDKMPANDEPOKSGKKPK----- 24

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OY 51 ELLQKNQNOEALQRAANS----- 69
DB 121 KLLQKNQNOEALQRAANSSESKRELKQIDITITRKLDEKSEKEOELLQONLOEALQ 180
OY 70 -----SESORELKIDITITRKLDEKSEKEOELLQONLOEALQRAANSFGPCQDWL 124
DB 181 KAKYSESORELKQIDITITRKLDEKSEKEOELLQONLOEALQRAANSFGPCQDWL 240
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DB 361 L 361

RESULT 3
ID 09XTA8 PRELIMINARY; PRT; 278 AA.
AC 09XTA8:
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE LECTIN-LIKE OXIDIZED LDL RECEPTOR.
GN LOX-1.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RA Sawamura T., Chen M.;
RT "Rabbit lectin-like oxidized LDL receptor 1.";
RT Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AB016237; BAA81912.1; -
DR InterPro: IPR001304; lectin_c.
DR Pfam: PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS50041; C_TYPE_LLECTIN_2; 1.
KW Receptor.
SQ SEQUENCE 278 AA; 31646 MW; 25A5E310F82A098 CRC64;

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OY 41 ---KLDEKSEKEOELLQONLOE-----ALQRAANSSESORELKIDITITRKLDEKSK 93
DB 63 QLLQVSDLLKQOQANLTQODHILEGQVLAQQAENASQSKRELKQIDITITRKLDEKSK 122
OY 94 EQEELLQKNQNOEALQRAANSFGPCQDWLWKRENCYLFGHPGWEKNQOTCSLGGOLQ 152
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OY 153 LLQINGADDLFTIIQAISSHTSPFWIGLHRRKPGQPLWENGTPLNFOFFTRGVSLQIY 212

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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 19, 2002, 19:24:00 : Search time 1864.41 Seconds  
(Without alignments)  
8350.815 Million cell updates/sec

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744  
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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues  
Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0  
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Post-processing: Minimum Match 0%  
Listing first 45 summaries

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- 7: gb\_ph:\*
- 8: gb\_pl:\*
- 9: gb\_pr:\*
- 10: gb\_ro:\*
- 11: gb\_sts:\*
- 12: gb\_sy:\*
- 13: gb\_un:\*
- 14: gb\_vi:\*
- 15: em\_ba:\*
- 16: em\_fun:\*
- 17: em\_hum:\*
- 18: em\_in:\*
- 19: em\_mu:\*
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- 31: em\_htg\_inv:\*
- 32: em\_htg\_other:\*
- 33: em\_htg\_inv:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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2	526.8	70.8	3750	10	AB005900	AB005900 Rattus no
3	298.2	40.1	1318	6	AR077718	AR077718 Sequence
4	298.2	40.1	1318	6	AR138263	AR138263 Sequence
5	298.2	40.1	1318	6	E12916	E12916 Human cDNA
6	298.2	40.1	1318	6	AF035776	AF035776 Homo sapi
7	298.2	40.1	2463	9	AB010710	AB010710 Homo sapi
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9	293.6	39.5	1578	4	AB018668	AB018668 Sus scrofa
10	287.2	38.6	1879	4	DB9049	DB9049 Bos taurus
11	287.2	38.6	1897	6	AR077716	AR077716 Sequence
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13	287.2	38.6	1897	6	E12914	E12914 Bovine cDNA
14	287.2	38.6	1906	6	AR077717	AR077717 Sequence
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21	108.4	14.6	169	10	AB018097S8	AB018104 Rattus no
22	106.2	14.3	162	10	AB018097S4	AB018100 Rattus no
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25	102	13.7	328	9	HSOLR3	AF079166 Homo sapi
26	102	13.7	15387	9	HSAL31757	AJ131757 Homo sapi
27	102	13.7	182211	2	AC024224	AC024224 Homo sapi
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## ALIGNMENTS

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DEFINITION Mus musculus oxidized LDL receptor (Lox-1) mRNA, complete cds.  
ACCESSION AF303744  
VERSION AF303744.1 GI:12006985  
KEYWORDS  
SOURCE  
ORGANISM  
house mouse.  
Mus musculus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE  
1 (bases 1 to 3763)  
Park, S.-H., Ahn, H.-J. and Cho, J.-J.  
TITLE Mouse Lox-1 is expressed in mast cells after Ige cross-linking  
JOURNAL Unpublished  
AUTHORS Park, S.-H., Ahn, H.-J. and Cho, J.-J.  
REFERENCE 2 (bases 1 to 3763)  
Park, S.-H., Ahn, H.-J. and Cho, J.-J.  
TITLE Direct Submission  
JOURNAL Submitted (07-SEP-2000) Microbiology, Kyung Hee University, College of Medicine, Dongdaemun-Gu, Hseki-Dong 1, Seoul, Korea

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Db	579	GCCCTGCAGAGAGCTGCAAACTCTTCAGAGAGATCCCAAGAGAACTCAAGGAAAGATA	638
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OY	304	aataagaacctccaagaagacccctgcacaagaagctgcacaacttccagcttcgtccaca	363
Db	699	AATCAGAACTCCCAAGAAAGCCCTTGCAAGAGTGCAAACTTTTCAGGTCTTGTCCACA	758
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Db	759	GACTGGCTCTGGCAATTAAGAAAACCTGTACCTTTCATGGGCCCCCTTTAGCTGGGAAAA	818
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OY	484	ctgaacatcatcttacaagaacatctcccataccactcccacttcttgaattgacat	543
Db	879	TTTGACATTTCATTTACAAAGCAATTTCCCATACCACTCCCGCTTGCGATTGGATTTGCAT	938
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OY	604	tttaagaaccaggggcgcttcttcaagctatatctcaagaagaactgtgcataacttcaa	663
Db	999	TTTTAAGACCAAGGGCGCTTTTTCACAGCATATATCTCAAGGCAACGTGCATACCTTCNA	1058

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VERSION		AB005900.1 GI:30777733	
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REFERENCE		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;	
AUTHORS		Rattus.	
TITLE		1 (bases 1 to 3750)	
JOURNAL		Fujita,T. Direct Submission Submitted (19-JUL-1997) Toshiro Fujita, University of Tokyo School of Medicine, Fourth Department of Internal Medicine; 3-28-6 Mejirodai, Bunkyo-Ku, Tokyo 112, Japan, Tokyo 112, Japan (E-mail:fujita-dis@n.tokyo.ac.jp, Tel:+81-3-3943-1151, Fax:+81-3-3942-5690)	
AUTHORS		2 (sites) Nagase,M., Hirose,S. and Fujita,T. Unique repetitive sequence and unexpected regulation of expression of rat endothelial receptor for oxidized low-density lipoprotein (LOX-1) Biochem. J. 330 (Pt 3), 1417-1422 (1998)	
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Oy	123 gctggacagaaatccaaagagcagagagcttctgcagatgatttcagacctccaaga	182		
Db	562 GCTGAATGGGATATCCAAAGACGACAGAGAGCTCTGCAGCAGAAATCAGAACTCCCAAGA	621		
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Db	622 AGCCCTGCGAAGAGGTGGAAATATTCAGAGAGAGTCCCGAAGAACTGTAAGAACAGAT	681		
Oy	243 agaacacctcaccttgaaagctgaacagagaatccaaagacagagagagcttcacaaga	302		
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Db	802 AGACTGGATCTGCGTAAAGAAAGTGTATTCCTTCCTGAGGCCCCCTTAACTGGGAAAA	861		
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	VERSION	AR077718.1	GI:10004464				
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REFERENCE		Unclassified.					
AUTHORS		1 (bases 1 to 1318)					
TITLE		Sawamura,T. and Masaki,T.					
JOURNAL		Recombinant production of human and bovine receptors for modified					
FEATURES		low-density lipoprotein					
source		Patent: US 5962260-A 5 05-OCT-1999;					
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Db	504	GAACTGGAATTCACCAAGAACACTGAAGAGATGACAAATTTGTCAAGCTCTGTTCGCA	563	
OY	363	agactgcctctgcacataaagaaactgtaacctctt---caatgggccccttgctggagaa	419	
Db	564	AGACTGGAATTCGCAATGAGAAACGTTACTATTTCCTGGGCTCATTTAACTGGGA	623	
OY	420	aaaaaacgggcagacctgccaalcctttgggtggccagttactacaataatggtgcaga	479	
Db	624	AAAGAGCCCAAGAGAAAGTCTGCTCTTGGATGCCAAGTGTGAAATTAATAGCACAGC	683	
OY	480	tgatctgcacattctctctccaagaacttcccataccacctcccatcttgattggatt	539	
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OY	540	gcatcggaagaagcctgcgcacaacatggtctatggaggaatggaaactccttgaattcca	599	
Db	744	GTCTCGGAGGAACCCACAGTACCAGTGGCTTGGGAGAGACGGTTCCTTTATATGCCCA	803	
OY	600	attccttaagaccagggcgcttctcttaacagctatattcatcaagaacactgctacacct	659	
Db	804	CTTATTTAAGTCCGAGGGCGTGTCTCCAGACATACCTTCAGGTACTGTGCATATAT	863	
OY	660	tcaagaacggagctgtgtctgtcgtaaaactgcgatcttaattgcattcagcatatgtcagaa	719	
Db	864	ACAACGAGAGAGCTGTTATGCGGAAACGATTTTAACTGCTTCAGTATATGTCCAGAA	923	
OY	720	gaagacaacatc	730	
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RESULT	4			
ARI38263	ARI38263	1318 bp	DNA	linear
LOCUS				
DEFINITION	Sequence 5 from patent US 6197937.			
ACCESSION	ARI38263			
VERSION	ARI38263.1	GI:14479772		

KEYWORDS : Unknown.  
 SOURCE : Unknown.  
 ORGANISM : Unknown.  
 REFERENCE : Unclassified.  
 1 (bases 1 to 1318)  
 AUTHORS : Sawamura,T. and Masaki,T.  
 TITLE : Modified low density lipoprotein receptor  
 JOURNAL : Patent: US 6197937-A 5 06-MAR-2001;  
 FEATURES : Location/Qualifiers  
 source 1..1318  
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QY 183 agccctgcagagagctgcgaacatcttcagagagagtcaccagagagactcaagggaagat 242  
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 DB 444 AGAACCCTTGCTCGAGCTGAATGAAATCCAAAGACAAATGGAACCTTCCACCA 503  
 QY 303 gaatcagaaccccaagagccctgcgaagagctgcgaacatcttcagctctgtccaca 362  
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 QY 660 tcaagacgagctgtgtctgcgaacatgcatcttaattgcatctcaagacatgacaga 719  
 DB 864 ACAACGAGAGCTGTATATCGGAAAACTCATTTAGTGCCTTCAGTATATGTCTAGAA 923  
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 DB 924 GAAGCAAAACC 934

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 E12916 1318 bp DNA linear PAT 24-JUN-1998  
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 DEFINITION Human cDNA encoding a denatured low-density lipoprotein receptor.  
 ACCESSION E12916  
 VERSION E12916.1 GI:3251747  
 KEYWORDS JP 1997098787-A/3.  
 SOURCE Homo sapiens.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 REFERENCE 1 (bases 1 to 1318)  
 AUTHORS Sawamura,T. and Masaki,T.

TITLE : MODIFIED LOW DENSITY LIPOPROTEIN RECEPTOR  
 JOURNAL : Patent: JP 1997098787-A 3 15-APR-1997;  
 COMMENT : NIPPON CHEMIPHAR CO LTD  
 OS Homo sapiens (human)  
 PN JP 1997098787-A/3  
 PD 15-APR-1997  
 PF 30-NOV-1995 JP 1995334234  
 PR 30-NOV-1994 JP 94P 321705, 31-JUL-1995 JP 95P 214206 PI  
 PC C12N15/09,C07H21/04,C07K14/705,C12P21/02,G01N33/53,G01N33/566,  
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 PC C12R1.91;  
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 CC topology: Linear;  
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QY 183 agccctgcagagagctgcgaacatcttcagagagagtcaccagagagactcaagggaagat 242  
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DEFINITION complete cds.
ACCESSION AF035776
VERSION AF035776.1 GI:3941299
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 2067)
AUTHORS Li,X., Bouzyk,M.M. and Wang,X.K.
TITLE Human oxidized low density lipoprotein receptor: characterization
of the full length cDNA sequence and assignment to human chromosome
12p13.1-12.3
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2067)
AUTHORS Wang,X.K.
TITLE Direct Submission
JOURNAL Submitted (24-NOV-1997) Cardiovascular Pharmacology, SmithKline
Beecham Pharmaceuticals, 709 Swedeland Road, UM2511, King of
Prussia, PA 19406, USA
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QY 183 agccctgcagagagctgtcaaaccttcagagagatcccaagagagagcaaggaagat 242
Db 304 AGCCCGCAACAGCAAGAGAGAGCTTCACAGAGTCACAAAACGACCAAGAAATGAT 363
QY 243 agaacaccctcaactgaagctgaacgagaaatccaagaagagagagctctacagaa 302
Db 364 AGAAACCTTCTGCTGGAAGATGAGAAATCCAAAAGCAAAATGGAATTCACACCA 423
QY 303 gaacacagagctccaagaagcctgcgaagagctgcgaacttcagctcttgccaca 362
Db 424 GAATCTGATATCCCAAGAAACACTGAAAGAGTACCAAAATTGTTAGCTCTTGCCGA 483
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QY 480 tgatcagatcattcttaccagaacttccaccaccccccattctgattgatt 539
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Db 844 GAAGCAAAACC 854
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DEFINITION cds.
ACCESSION AB010710 D89050
VERSION AB010710.1 GI:2828355
KEYWORDS lectin-like oxidized LDL receptor; LOX-1.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 2463)
AUTHORS Sawamura,T.
TITLE Direct Submission
JOURNAL Submitted (22-JAN-1998) Tatsuya Sawamura, Kyoto University,
Department of Pharmacology, Faculty of Medicine, Yoshidakonoe-cho,
Sakyo-ku, Kyoto, Kyoto 606, Japan
(E-mail:sawamura@four.med.kyoto-u.ac.jp, Tel:81-75-753-4393,
Fax:81-75-753-4402)
2 (sites)
REFERENCE Sawamura,T., Kume,N., Aoyama,T., Moriwaki,H., Hoshikawa,H.,
AUTHORS Alba,Y., Tanaka,T., Miwa,S., Katsura,Y., Kita,T. and Masaki,T.
TITLE An endothelial receptor for oxidized low-density lipoprotein
JOURNAL Nature 386 (6620), 73-77 (1997)
MEDLINE 97205278
COMMENT On Feb 3, 1998 this sequence version replaced gi:1902983.
D89050: Submitted (12-Nov-1996).
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BASE COUNT 734 a 518 c 467 g 744 t
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Query Match 40.1%; Score 298.2; DB 9; Length 2463;

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Best Local Similarity 72.6%; Pred. No. 1.4e-72;  
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RESULT 8
LOCUS BC022295 2480 bp mRNA linear PRI 04-FEB-2002
DEFINITION Homo sapiens, oxidised low density lipoprotein (lectin-like)
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ACCESSION BC022295.1 GI:18490152
VERSION 1
KEYWORDS MGC.
SOURCE human.
ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 2480)
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL Submitted (01-FEB-2002) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT Contact: MGC help desk
            Email: gcgaps@email.nih.gov
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            cDNA Library Preparation: CLONTECH Laboratories, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Sequencing Group at the Stanford Human Genome
            Center, Stanford University School of Medicine, Stanford, CA 94305
            Web site: http://www.shgc.stanford.edu
            Contact: (Dickson, Mark) mcdexall.stanford.edu

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Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers, R. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>  
Series: IRAL Plate: 37 Row: F Column: 6  
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ACCESSION	AB018668							
VERSION	AB018668.1	GI:6682817						
KEYWORDS	lectin-like oxidized LDL receptor-1.							
SOURCE	Sus scrofa	aortic endothelial cells cDNA to mRNA.						
ORGANISM	Sus scrofa							
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AUTHORS	1 (states)							
TITLE	Chen, M., Narumiya, S., Masaki, T., and Sawamura, T.							
JOURNAL	Conserved C-terminal residues within the lectin-like domain of							
MEDLINE	Biochem. J. 355 (Pt 2), 289-296 (2001)							
REFERENCE	2 (bases 1 to 1578)							
AUTHORS	Sawamura, T.							
TITLE	Direct Submission							
JOURNAL	Submitted (14-OCT-1998) Tatsuya Sawamura, National Cardiovascular							
	Center Research Institute, Department of Bioscience, 5-7-1							
	Fushihrodai, Suita, Osaka 565-8565, Japan							
	(E-mail:sawamura@ri.ncvc.go.jp, Tel:81-6-833-5012ext.2518),							
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Db	662	ATCTGTGAGGAACCAACCAACAACTCATGGGCTCTGGAGGACGGTACTCCTTTGATGCCCCA	721
Oy	600	attctttaagacccaagggcgctttcttcaagctatattcatcaagaacatgylacact	659
Db	722	CTTGTTTAGACTCCAGCGAGCTGCTTCCCAATGTATCCTTCACAGCACCTTGCGTATAT	781
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D89049	DEFINITION	Bos taurus mRNA for lectin-like oxidized LDL receptor, complete cds.	1879 bp	linear
D89049	ACCESSION			MAM 07-FEB-1999
D89049.1	VERSION	GI:1902981		
D89049.1	KEYWORDS	lectin-like oxidized LDL receptor; LOX-1.		
Bos taurus	SOURCE	Bos taurus aortic endothelial cells cDNA to mRNA, clone:pBLOX-1.		
ORGANISM		Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea; Bovidae; Bovinae; Bos.		
REFERENCE		1 (bases 1 to 1879)		
AUTHORS		Sawamura,T.		
TITLE		Direct Submission		
JOURNAL		Submitted (12-NOV-1996) Tatsuya Sawamura, Kyoto University, Department of Pharmacology, Faculty of Medicine; Yoshida-konocho, Sakyo-ku, Kyoto, Kyoto 606, Japan (E-mail:sawamura@med.kyoto-u.ac.jp, Tel:+81-75-753-4477, Fax:+81-75-753-4402) 2 (bases 1 to 1879)		
REFERENCE		Sawamura,T., Kume,N., Aoyama,T., Moriaki,H., Hoshikawa,H., Alpha.Y., Tanaka,T., Miwa,S., Katsura,Y., Kita,T. and Tomoh.M. A novel endothelial receptor for oxidized low density lipoprotein unpublished (1996)		
TITLE		3 (sites)		
JOURNAL		Sawamura,T., Kume,N., Aoyama,T., Moriaki,H., Hoshikawa,H., Alpha.Y., Tanaka,T., Miwa,S., Katsura,Y., Kita,T. and Masaki.T. An endothelial receptor for oxidized low-density lipoprotein Nature 386 (6620), 73-77 (1997)		
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AUTHORS				
TITLE				
JOURNAL				
FEATURES				
MEDLINE				
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Qy      363 agactgctctgcatlaaagaanaactgttacc---tcttcattgggccccttgctggga 419
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Qy      720 gaagacaatcattctg 735
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LOCUS   E12914      1897 bp      DNA      linear      PAT 24-JUN-1998
DEFINITION Bovine cDNA encoding a denatured low-density lipoprotein receptor.
ACCESSION E12914
VERSION   E12914.1 GI:3251745
KEYWORDS  JP 1997098787-A/1.
SOURCE    cow.
ORGANISM  Bos taurus
           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
           Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
           Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 1897)
AUTHORS  Sawamura,T. and Masaki,T.
TITLE     MODIFIED LOW DENSITY LIPOPROTEIN RECEPTOR
JOURNAL   Patent: JP 1997098787-A 1 15-APR-1997;
           NIPPON CHEMIPHAR CO LTD
COMMENT   OS Bos taurus (bovine)
           PN JP 1997098787-A/1
           PD 15-APR-1997
           PE 30-NOV-1995 JP 1995334234
           PR 30-NOV-1994 JP 94P 321705, 31-JUL-1995 JP 95P 214206 PI
           SAAMURA TATSUYA, MAZAKI TOMOO
           PC C12N15/09,C07H21/04,C07K14/705,C12P21/02,G01N33/53,G01N33/566,
           PC C12P21/02,
           PC C12R1:91;
           CC strandedness: Double;
           CC topology: Linear;
           FH Key
           FH Location/Qualifiers
           FT source
           FT 1.1897
           FT /organism='Bos taurus'
           FT /cell_type='vascular endothelial cells' FT

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FEATURES
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Location/Qualifiers
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ORIGIN

Query Match      38.6%; Score 287.2; DB 6; Length 1897;
Best Local Similarity 71.0%; Freq. No. 1.7e-69;
Matches 395; Conservative 0; Mismatches 158; Indels 3; Gaps 1;

Qy      183 agccctcgagagagctgcaactcttcagagagctcccaagagagactcaagaagaat 242
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Qy      243 agacacccctcaacttgaaagctgaacgagaaatccaaagacgagagagctctacaaga 302
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Qy      303 gaatagaacctccaagaagacccctgcaagaagctgcaacttctcaagctctgctcaca 362
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Qy      363 agactgctctgcatlaaagaanaactgttacc---tcttcattgggccccttgctggga 419
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Qy      420 aaaaacccgagagacctgccaactcttggtgggccaagtactacaataatggtgcaga 479
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DEFINITION Sequence 3 from patent US 5962260.
ACCESSION AR077717
VERSION   AR077717.1 GI:10004463
KEYWORDS
SOURCE    Unknown.
ORGANISM  Unknown.
REFERENCE 1 (bases 1 to 1906)
AUTHORS  Sawamura,T. and Masaki,T.
TITLE     Recombinant production of human and bovine receptors for modified

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GenCore version 4.5  
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

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(Without alignments)  
6049.940 Million cell updates/sec

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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 1736436 seqs, 858457221 residues  
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Listing first 45 summaries

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## SUMMARIES

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4	298.2	40.1	2463	22	AAH90651
5	298.2	40.1	2468	22	AAH47105
6	293.6	39.5	1578	22	AAH47113
7	287.2	38.6	1335	20	AAH8529
8	287.2	38.6	1879	22	AAH47106
9	287.2	38.6	1897	17	AAT32576

10	287.2	38.6	1897	20	AAH8528	Bovine LDL recepto
11	287.2	38.6	1906	17	AAT32577	Low density lipopr
12	287.2	38.6	1921	20	AAH8530	Bovine LOX-1 extra
13	277.6	37.3	1514	22	AAH47112	O. cuticulus LOX-1
14	203.8	27.4	540	22	AAL25166	Human breast cance
15	161.6	21.7	532	21	AAA45084	Human secreted exp
16	100.2	13.5	2450	22	AAH03910	Human secreted pro
17	96.2	12.9	497	22	AAL16323	Human breast cance
18	74.4	10.0	741	20	AAH01260	Human DC3' protein
19	74.4	10.0	1018	20	AAH07533	Human SPCMP4 polyp
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23	72.4	9.7	2477	20	AAH234287	Human PRO1082 nucl
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25	72.4	9.7	2478	22	AAH45978	Human DNA encoding
26	66	8.9	2645	22	AAH31262	Human cDNA encoding
27	61.2	8.2	528	19	AAH42551	Mouse dec1n-1 ext
28	61.2	8.2	2298	19	AAH42548	Mouse dec1n-1 cdn
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31	48	6.5	4000	18	AAT91902	Mannose-1-phosphat
32	45.2	6.1	5661	19	AAH21518	Rattus norvegicus
33	44.8	6.0	693	23	AAH74240	DNA encoding novel
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35	44.8	6.0	6432	23	AAH55903	DNA encoding novel
36	44.8	6.0	7516	22	AAH51987	Human polynucleoti
37	44.8	6.0	8486	22	AAH52971	Human polynucleoti
38	44	5.9	1542	21	AAH27055	Human cell surfaci
39	44	5.9	3773	21	AAH18028	Lung cancer associ
40	43.6	5.9	1080	24	AB19537	Mouse ischaemic co
41	42.4	5.7	1869	23	AAH6785	DNA encoding novel
42	42.4	5.7	3234	12	AAH05019	Encodes mouse bull
43	41.8	5.6	340	14	AAH037296	DNA encoding SSP-5
44	41.8	5.6	1808	22	AAH02460	Mouse PEP7A cDNA c
45	41.6	5.6	6607	22	AAH98321	Rabbit EST-derived

## ALIGNMENTS

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DT	30-NOV-2001 (first entry)
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DE	Rat LOX-1 polypeptide encoding cDNA.
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KM	LOX-1; LDL: monoclonal antibody; low density lipoprotein; human;
KW	atherosclerosis; cardiovascular; kidney disease; inflammatory disorder;
OS	leukocyte; rat; ss.
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OS	Rattus norvegicus.
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PD	07-SEP-2001.
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PF	02-MAR-2001; 2001WO-JP01636.
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PR	02-MAR-2000; 2000JP-0057745.
PR	31-OCT-2000; 2000JP-0333116.



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XX 10-SEP-1999 (first entry)
DE Human LDL receptor encoding DNA.
KW Human; LDL; denatured; oxidised; arteriosclerosis; hyperlipidaemia;
KW low density lipoprotein; receptor; detection; immunoglobulin;
KW fusion protein; ss.
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XX Homo sapiens.
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XX FT 949..1318
XX FT 3'UTR /*tag= c
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XX PE 18-DEC-1998; 98WO-JP05744.
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XX PR 16-DEC-1998; 98JP-0358170.
XX PR 19-DEC-1997; 97JP-0364981.
XX PR 09-DEC-1998; 98JP-0349648.
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XX PA (NTSB ) JAPAN TOBACCO INC.
XX
XX PI Kakutani M, Masaki T, Sawamura T;
XX
XX WPI: 1999-416906/35.
XX
XX P-PSDB; AAY24151.
DR
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XX
XX Fusion peptide for assay of oxidized LDL and for therapeutic use
XX
XX PS Disclosure: Page 84-87; 105pp; Japanese.
XX
XX CC The present invention describes a fusion peptide which consists of the
XX CC extracellular domain of a mammalian oxidized LDL (low density
XX CC lipoprotein) receptor, fused to a partial heavy chain of a mammalian
XX CC immunoglobulin containing all or part of the constant region. Oxidized
XX CC LDL is a denatured form of LDL occurring in patients having
XX CC arteriosclerosis or hyperlipidaemia, and the fusion peptide can be
XX CC used for the assay of oxidized LDL in biological samples from such
XX CC patients, for the diagnosis of the disorders. It can also be used
XX CC therapeutically for the prevention and treatment of arteriosclerosis and
XX CC hyperlipidaemia. The present sequence encodes the human LDL receptor.
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XX SQ Sequence 1318 BP; 366 A; 306 C; 286 G; 360 T; 0 other;
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Best Local Similarity 72.6%; Pred. No. 1,1e-76;
Matches 400; Conservative 0; Mismatches 148; Indels 3; Gaps 1;
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QY 720 gaagacaact 730
DB 924 gaaggcaaac 934

RESULT 4
AAF90651
ID AAF90651 standard; DNA; 2463 BP.
AC AAF90651;
XX
XX 04-MAY-2001 (first entry)
XX
XX Human secreted protein encoding DNA, SEQ ID NO:120.
DE
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XX Secreted protein; transmembrane protein; human; drug screening;  
 KW activity modulator; expression modulator; cancer; immunological disorder;  
 KM cytosolic; immunomodulatory; gene therapy; ds.  
 XX  
 OS Homo sapiens.  
 PN WO200109162-A2.  
 PD 08-FEB-2001.  
 XX  
 PF 31-JUL-2000; 2000MO-US20935.  
 XX  
 PR 30-JUL-1999; 99US-0365164.  
 XX  
 PA (MILL-) MILLENNIUM PHARM INC.  
 PI Fraser CC, Sharp JD, Kirst SJ, Barnes TM, Wrighton N, Myers PS;  
 PI Pan Y;  
 DR WPI; 2001-138647/14.  
 XX  
 XX Nucleic acids encoding secreted TANGO and MANGO polypeptides, useful  
 PT for the prevention, diagnosis and treatment of, e.g. cancers and immune  
 PT disorders -  
 PS Disclosure; Page 272; 332pp; English.  
 XX  
 XX The invention relates to novel secreted/transmembrane proteins, and  
 CC nucleic acids encoding them. The novel proteins are designated TANGO 339,  
 CC TANGO 353, TANGO 358, TANGO 365, TANGO 368, TANGO 369, TANGO 383, TANGO  
 CC 393, TANGO 402, MANGO 346 and MANGO 349 and are of human origin, and a  
 CC murine TANGO 393 is also included within the scope of the invention. The  
 CC invention also encompasses fragments and variants of the proteins of the  
 CC invention, and nucleic acids encoding them. The invention additionally  
 CC relates to host cells comprising a nucleic acid of the invention; methods  
 CC for the production of a protein of the invention; an antibody specific  
 CC for a protein of the invention; methods for detecting a protein or  
 CC nucleic acid of the invention; and methods of identifying agents which  
 CC bind to or modulate the activity of a protein of the invention. The novel  
 CC secreted proteins, nucleic acids encoding them, and antibodies against  
 CC them may be used in the prevention, diagnosis and treatment of diseases  
 CC associated with inappropriate expression or activity of the secreted  
 CC proteins. The secreted proteins of the invention may also be used to  
 CC identify modulators of expression or activity, which may be useful in  
 CC the treatment of disorders associated with the proteins of the  
 CC invention e.g., cancers and immunological disorders. The present  
 CC sequence represents DNA encoding a human secreted protein.  
 X  
 X Sequence 2463 BP; 734 A; 518 C; 467 G; 744 T; 0 other;

Query Match 40.1%; Score 298.2; DB 22; Length 2463;  
 Best Local Similarity 72.6%; Pred. No. 1.5e-76;  
 Matches 400; Conservative 0; Mismatches 148; Indels 3; Gaps 1;

QY 183 agccctgcagagagctgcgaactcttcagagagctccagagagaactcaagggaagat 242  
 DB 319 agcccgcaacaagaagagcttcacagagctcagaaacgaactcaagaatgat 378  
 QY 243 agacaccctcacttggaagtgaagagaaatccaaagagcagagagcttcaagaa 302  
 DB 379 agaaacctgtcgcgaagctgaatgaatccaaagagcaatggaacttaccacca 438  
 QY 303 gaatcagaacctcagaagccctgcgaagagctgcaaaacttcagctcgtccaca 362  
 DB 439 gaatcgaatctcagaagaacctgaagagagtagcaaatgttcagctcgtccgca 498  
 QY 363 agactgctcgtgcataaagaactgttaacctt--ccatgggccccttggctggga 419  
 DB 499 agactgactcgtgcagagaaactgttaccatttctcgtggcatttaacttggga 558  
 QY 420 aaaaaaccggcagagctgcgaatcttgggtggccaggttactacaaatgaatgtcaga 479

DB 559 aaagagccaagagagagctgtcttcttgcgaatgtcgaatgaatcaatcagcagc 618  
 QY 480 tgaatcgaatcttcaatcaagaattcccaatcccaactcccaactcgtgattgatt 539  
 DB 619 tgatctggaacttcaatccagagaagcaatttccattccagtttccattcgtatgggct 678  
 QY 540 gcatcgaagaagcgtctgcgaacatgagctatgggaatgaaactccttgaatttca 599  
 DB 679 gtctcgagagaaccccatgctcgtggaagcgttctccttggatcccca 738  
 QY 600 atcttcaagaacaggggcttcttcttcaagcctatctcaagaacgtgtcatcct 659  
 DB 739 ctatttaagatccgagcgctgtctccagacataccctcaggtacccgtgcataat 798  
 QY 660 tcaagcagagcgtgtgtcgtgaaactgcatctaatcattcagatgcagaa 719  
 DB 799 acaacgagagagcgtttatgcgaaactgcatlittgctgcttcagatatatgcagaa 858  
 QY 720 gaagacaatc 730  
 DB 859 gaagcacaacc 869

RESULT 5  
 AAH47105  
 ID AAH47105 standard; cDNA; 2468 BP.  
 XX  
 XX AAH47105;  
 AC XX  
 DT 30-NOV-2001 (first entry)  
 XX  
 DE Human LOX-1 polypeptide encoding cDNA.  
 XX  
 KW LOX-1; LDL; monoclinal antibody; low density lipoprotein; human;  
 KM atherosclerosis; cardiovascular; kidney disease; inflammatory disorder;  
 KW leukocyte; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT 5'UTR 1..61  
 FT CDS 62..863  
 FT /\*tag- a  
 FT /\*tag- b  
 FT 3'UTR 884..2468  
 FT /\*tag- c  
 XX  
 PN WO200164862-A1.  
 XX  
 PD 07-SEP-2001.  
 XX  
 PF 02-MAR-2001; 2001MO-JP01636.  
 XX  
 PR 02-MAR-2000; 2000JP-0057745.  
 XX  
 PR 31-OCT-2000; 2000JP-033116.  
 XX  
 PA (ABGE-) ABGENIX INC.  
 PI Kobayashi Y, Tsuji H, Kamada M, Sawamura T;  
 DR WPI; 2001-565503/63.  
 DR P-PSDB; AAB85869.  
 XX  
 PT Human monoclonal antibodies recognizing oxidized low density  
 PT lipoprotein receptor for treatment of atherosclerosis and  
 PT cardiovascular and kidney diseases -  
 XX  
 PS Disclosure; Page 87-92; 131pp; Japanese.  
 XX  
 XX The invention provides human monoclonal antibodies and their fragments  
 CC binding to human oxidized low density lipoprotein (LDL) receptor (LOX-1),  
 CC and inhibiting intracellular binding of the receptor to oxidized LDL.



FT	3' UTR	/*tag= b
FT		870..1578
FT		/*tag= c
XX		
PN	WO200164862-A1.	
XX		

02-MAR-2001: 2001WO-JP01636.  
02-MAR-2000: 2000JP-0057745.

XX (ABGE-) ABGENIX INC.  
PA  
XX  
XX  
PI Kobayashi Y, Tsuji H, Kamada M, Sawamura T;  
XX  
XX WPT; 2001-565503/63.  
DR P-PSDB; AAB85872.  
XX  
XX  
XX Human monoclonal antibodies recognizing oxidized low density  
PI lipoprotein receptor for treatment of atherosclerosis and  
PT cardiovascular and kidney diseases -  
XX  
PS Disclosure; Page 111-115; 131pp; Japanese.

XX The invention provides human monoclonal antibodies and their fragments  
CC binding to human oxidized low density lipoprotein (LDL) receptor (LOX-1),  
CC and inhibiting intracellular binding of the receptor to oxidized LDL.  
CC Drug compositions containing the Mab are useful in the treatment and  
CC prevention of atherosclerosis, cardiovascular and kidney diseases,  
CC inflammatory disorders and infiltration of leukocytes. The present  
CC sequence represents a 5' scrofa LOX-1 polypeptide encoding cDNA.  
XX  
XX Sequence 1578 BP: 415 A; 351 C; 321 G; 491 T; 0 other;

Query Match	39.5%;	Score 293.6;	DB 22;	Length 1578;
Best Local Similarity	71.8%;	Pred. No. 2,6e-75;		
Matches_399; Conservative	0;	Mismatches 154;	Indels 3;	Gaps 1;
QY	183	agccctgcagagagctgcacactcttcagagagagctccacagagaactcaaggaagaat	242	
Db	302	agccacagcgccacgagcggaanaaatctccacagagagtcacaaaggaactacagaatgat	361	
QY	243	agacacaccctcacacttgaagctgaacgagagaaatccaaagcgagggagagcttcacaga	302	
Db	362	agaaacatcttgcacacaatctgatagaaataccacagaacacgatggagcttcaacaga	421	
QY	303	gagtcagaacctccacagaagaccccttcacaaagagcttcaaacctttcaagctcttgcaca	362	

QY 363 aagactgacctgcatagaagaactgttac---ctcttcacatggcccttgctggaga 419  
|||||  
Db 482 agactggcccttgcatagaagaactggttaacaatttctctctggcccaatttagttggaga 541  
QY 420 aaaaaacccgacagacctgccaactctttggttggccagttaccacaaatbaatggtgcaga 479  
|||||  
Db 542 aaaaagccgggagactgcttctcttggatgcccacactgcgtgaagattaatagcagaga 601  
QY 480 tgaatcgcaattcatatcttcaagaagaatttcccatcacactcccatcttgattggatt 539  
|||||  
Db 602 cgatctcggaattcatccacagaacaacatcgcccatctccatcttccttgatggatggatt 661  
QY 540 gcatcggaagaagctctgccaacacatgctatggtggaatggaactccttgaatttca 599  
|||||  
Db 662 atctctggagaaacccaacaactcatgctctggagagacggtactcccttatbcccaca 721  
QY 600 attcttcaagacacaggagcgcttctctttaaagtatattcatcaagaacatggtcacact 659  
|||||  
Db 722<ctgttttaactccacagagcgctctcccaaatgtatctctcaagcactgtgcgtatat 781

QY 660 tcaagacgagctgtctgctgaacatgcattcttaattgcattcgcgcatatgtcagaa 719  
 Db 782 acacagggagatgtttcttgtaaacatgcatttaaatgattcagatatagttcagaa 841  
 QY 720 gaagacaatcatttg 735  
 Db 842 gaaggcgaaatcctctg 857

## RESULT 7

AAH8529  
 ID AAX8529 standard; DNA: 1335 BP.

AC AAX8529;

DT 10-SEP-1999 (first entry)

DE Bovine LOX-1 extracellular region/human IgG1 Fc region chimeric protein.

KW LDL; denatured; oxidised; arteriosclerosis; hyperlipidaemia;

KM low density lipoprotein; receptor; detection; immunoglobulin;

XX fusion protein; chimeric protein; ss.

OS Chimeric - Bos sp.

XX Chimeric - Homo sapiens.

PN WO932520-A1.

PD 01-JUL-1999.

PF 18-DEC-1998: 98WO-JP05744.

XX 16-DEC-1998: 98JP-0358170.

PR 19-DEC-1997: 97JP-0364981.

PR 09-DEC-1998: 98JP-0349648.

XX (NISR) JAPAN TOBACCO INC.

PA Rakutan M, Masaki T, Sawamura T;

XX WPI: 1999-418906/35.

DR P-PSDB: AAY24153.

XX Fusion peptide for assay of oxidized LDL and for therapeutic use

PT Claim 14: Page 79-83; 105pp: Japanese.

PS The present invention describes a fusion peptide which consists of the

XX extracellular domain of a mammalian oxidized LDL (low density

CC lipoprotein) receptor, fused to a partial heavy chain of a mammalian

CC immunoglobulin containing all or part of the constant region. Oxidized

CC LDL is a denatured form of LDL occurring in patients having

CC arteriosclerosis or hyperlipidaemia, and the fusion peptide can be

CC used for the assay of oxidized LDL in biological samples from such

CC patients for the diagnosis of the disorders. It can also be used

CC therapeutically for the prevention and treatment of arteriosclerosis and

CC hyperlipidaemia. The present sequence encodes a chimeric protein

CC comprising the bovine LOX-1 extracellular region and the human

CC immunoglobulin IgG1 Fc region.

XX Sequence 1335 BP; 372 A; 371 C; 324 G; 268 T; 0 other;

SO Query Match 38.6%; Score 287.2; DB 20; Length 1335;

Best Local Similarity 71.0%; Pred. No. 1.8e-73;

Matches 395; Conservative 0; Mismatches 158; Indels 3; Gaps 1;

QY 183 agcctgcagagagctgcgaactcttcagagaggtccacagagaactcaaggaagat 242

Db 66 agccagcgagcagcaaaatctgcagagaggtccacagagaactcaaggaagat 125

QY 243 agnaccctcacttgatgaagagaatcccaagagcagagagcttctacagaa 302

Db 126 agaaaccccttgccacaaagctggaatgagaatcccaagaactaaatgaaacttcacgca 185  
 QY 303 gaatcagaacctccaagaagagctgcgaagaagctgcgaactttcaagttccatccaca 362  
 Db 186 gaacttgaatctccaagaagatctgaaagagcagcaactatcagttccttcccca 245  
 QY 363 agactgctctgagcaataaagaactgttaccc--tcttcattggcccttggctggga 419  
 Db 246 agactgctctgagcaataaagaactgttacccaatttcccttggcttcttaattggga 305  
 QY 420 aaaaacccgagagccctgcgaactcttgggtggccagttactaaatgaattgagcaga 479  
 Db 306 aaaaacccgagagagctgttcttggatgagccacttgcgaagatlaagacacaga 365  
 QY 480 tgatctacatctcattcaagaatctccacacactccacacttgcgaatgagat 539  
 Db 366 tgaacttgaatctcattcaagaatctccacacacttgcgaatgagatgagat 425  
 QY 540 gcatcggaagaagcctgccaacacatgagctatggagaaatggaactccttgaatttca 599  
 Db 426 gcatatgagaagaacccaattactcgtgcttggagaaatggtactccttgcagcccca 485  
 QY 600 attcttaagaacagagggcgttcttcttaagctatattcacaagcaactgtagatcct 659  
 Db 486 ctgtttagaattcaaggagcgttcttccgtatgataccttcaggagcctgtagatcct 545  
 QY 660 tcaagacgagctgtctgcctgaagaactgcattcttaattgcattcagcatatgtcagaa 719  
 Db 546 tcaagagggagagctgttcttgcgaagaactgcatttcaactgcattcagcatatgtcagaa 605  
 QY 720 gaagacaatcatttg 735  
 Db 606 gaaggcgaaatcctctg 621

## RESULT 8

AAH47106

ID AAH47106 standard; cDNA; 1879 BP.

AC AAH47106;

DT 30-NOV-2001 (first entry)

XX Bovine LOX-1 polypeptide encoding cDNA.

DE LOX-1; LDL; monoclonal antibody; low density lipoprotein; human;

XX atherosclerosis; cardiovascular; kidney disease; inflammatory disorder;

KM Leukocyte; bovine; ss.

OS Bos taurus.

XX Key Location/Qualifiers

FT 5'UTR 1..34

FT CDS /\*tag= a

FT 3'UTR /\*tag= b

FT /\*tag= c

XX WO200164862-A1.

PD 07-SEP-2001.

PF 02-MAR-2001; 2001WO-JP01636.

PR 02-MAR-2000; 2000JP-0057745.

PR 31-OCT-2000; 2000JP-0331116.

PA (ABGE-) ABGENIX INC.

PI Kobayashi Y, Tsuji H, Kamada M, Sawamura T;

DR WPI: 2001-565503/63.





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FH Key Location/Qualifiers
FT 5'UTR 1..34
FT CDS 35..856
FT 3'UTR 857..1906
FT polyA_signal 1868..1873
FT misc_feature 1889..1906
FT /tag= b
FT /product= LDL_receptor
FT /tag= c
FT /tag= d
FT /tag= e
FT /note= "polyA site"
XX
XX MO617058-A1.
XX
XX 06-JUN-1996.
XX
XX 30-NOV-1995; 95WO-JP02444.
XX
XX 31-JUL-1995; 95JP-0214206.
XX 30-NOV-1994; 94JP-0321705.
XX
XX (NICM ) NIPPON CHEMIPHAR CO.
XX
XX Masaki T, Sawamura T;
XX
XX WPI: 1996-277778/28.
XX P-PSDB: AAR99857.
XX
XX DNA encoding denatured low-density lipoprotein receptor of mammalian
XX haemangioendothelial cells - useful for generating antibodies for
XX use in detection of LDL in biological samples
XX
XX Claim 1; Page 27-30; 44pp; Japanese.
XX
XX The present sequence is that of a bovine DNA which encodes a denature low
XX density lipoprotein (LDL) receptor isolated from haemangioendothelial
XX cells. The DNA is useful for the production of the receptor protein in
XX transformed hosts. Antibodies to the protein are useful in detection
XX and assays of LDL in biological samples.
XX
XX Sequence 1906 BP; 541 A; 351 C; 355 G; 659 T; 0 other;
XX
Query Match 38.6%; Score 287.2; DB 17; Length 1906;
Best Local Similarity 71.0%; Pred. No. 2,1e-73;
Matches 395; Conservative 0; Mismatches 158; Indels 3; Gaps 1;
QY 183 agccctgcagagagctgcgaactcttcagagagccagagagactccaagggaagat 242
DB 289 agccacagccgcagatcagaataatctgccagagatcacagaagaactccaagaatgat 348
QY 243 agacacccctcaacttgaaagctgaacgagaatcccaagaagcagagagctctacaga 302
DB 349 agaacccttgcccaacagctgagatgaataatccaagaataatgacttaccgcga 408
QY 303 gaatcagaactccaagaagccctgcgaagagctgcgaactttcattctctgcacaa 362
DB 409 gaactggaatccaagaagactctcgaagagcagcaactatctaagctctctcccca 468
QY 363 agactgctcgcgataaagaagaactgtacc---tcttcattggcccttgctggtgga 419
DB 469 agactgctcgcgataaagaagaactgtaccatttccctctgctctttaaattggga 528
QY 420 aaaaaacgcgagactgcgaactcttggtggtgcagttactacaataatggtgcaga 479
DB 529 aaaaaacgcgagactgcgtcttggtggtgcagttactacaataatggtgcaga 588
QY 480 tgatcgcattcattctacaaagcaattccatccacccctccattctgattgatt 539
DB 589 tgaactggaattcaccagcaaatgattgcccattccctctctgattggtgatt 648

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QY 540 gcatcgagaagcctgcacacatggtatggagaaatggaactccttgaattcca 599
DB 649 gtcaatggagaaacccaattactcgtgcttgggaagaatggtactccttgaagcccca 708
QY 600 attccttaagaccagggcgttcttcaacgcatatcatccaagaactggtacact 659
DB 709 ctgtttgaattcagagagcgtgttcccgatgatactcctcaggaactggtacataat 768
QY 660 tcaagacggagctgtgtcgtcgtgaagaacttcttaattgattcagcatatgcaaga 719
DB 769 tcaagagggaactgttctgtcgtgaagaacttcttaactgcatcagtatatgtcaaaa 828
QY 720 gaagacaatacatctg 735
DB 829 gaagcgcaatcatctg 844

RESULT 12
AAK88530
ID AAK88530 standard; DNA: 1921 BP.
XX
XX AAK88530;
XX
XX 10-SEP-1999 (first entry)
XX
XX Bovine LOX-1 extracellular region/human IgG1 Fc region chimeric protein.
XX
XX LDL; denatured; oxidised; arteriosclerosis; hyperlipidaemia;
XX low density lipoprotein; receptor; detection; immunoglobulin;
XX fusion protein; chimeric protein; ss.
XX
XX Chimeric - Bos sp.
XX
XX Chimeric - Homo sapiens.
XX
XX WO9932520-A1.
XX
XX 01-JUL-1999.
XX
XX 18-DEC-1998; 98WO-JP05744.
XX
XX 16-DEC-1998; 98JP-0358170.
XX 19-DEC-1997; 97JP-0364981.
XX 09-DEC-1998; 98JP-0349648.
XX
XX (NISB ) JAPAN TOBACCO INC.
XX
XX Kakutani M, Masaki T, Sawamura T;
XX
XX WPI: 1999-418906/35.
XX P-PSDB: AAY24153.
XX
XX Fusion peptide for assay of oxidized LDL and for therapeutic use
XX
XX Claim 14; Page 98-102; 105pp; Japanese.
XX
XX The present invention describes a fusion peptide which consists of the
XX extracellular domain of a mammalian oxidized LDL (low density
XX lipoprotein) receptor, fused to a partial heavy chain of a mammalian
XX immunoglobulin containing all or part of the constant region. Oxidized
XX LDL is a denatured form of LDL occurring in patients having
XX arteriosclerosis or hyperlipidaemia, and the fusion peptide can be
XX used for the assay of oxidized LDL in biological samples from such
XX patients, for the diagnosis of the disorders. It can also be used
XX therapeutically for the prevention and treatment of arteriosclerosis and
XX hyperlipidaemia. The present sequence encodes a chimeric protein
XX comprising the bovine LOX-1 extracellular region and the human genomic
XX DNA immunoglobulin IgG1 Fc region.
XX
XX Sequence 1921 BP; 479 A; 592 C; 481 G; 369 T; 0 other;
XX
Query Match 38.6%; Score 287.2; DB 20; Length 1921;
Best Local Similarity 71.0%; Pred. No. 2,1e-73;

```

Matches 395; Conservative 0; Mismatches 158; Indels 3; Gaps 1;

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QY 183 agccctgcagagagctgcgaactcttcagaagagctcccaagagaactcaaggaagat 242
    ||||| || || || || || || || || || || || || || || || || || || ||
DB 66 agccagcgcgcagtcagaaaaatctgcagagctcacagaagaactcaagaatgat 125
    ||||| || || || || || || || || || || || || || || || || || || ||
QY 243 agacaccccttcagcttgaaagtgaaatccaaagacagagagagctttacagaa 302
    ||||| || || || || || || || || || || || || || || || || || || ||
DB 126 agaaacccctgcacaaagcttgatgaatccaaagaaactaatgaacttcacgcga 185
    ||||| || || || || || || || || || || || || || || || || || || ||
QY 303 gaatcagaactccaaagacccctgcgaagagctgcgaacttcagctcgtccaca 362
    ||||| || || || || || || || || || || || || || || || || || || ||
DB 186 gaacccgaatctccaaagagcttcgaagagagcagaacaaactacgtctgtcccca 245
    ||||| || || || || || || || || || || || || || || || || || || ||
QY 363 agactgctctgcgcataaagaaactgttac--tcttcacatgggccccttgctggga 419
    ||||| || || || || || || || || || || || || || || || || || || ||
DB 246 agactgctctgcgcataaagaaactgttacaaatttctcctcgtccttttaattggga 305
    ||||| || || || || || || || || || || || || || || || || || || ||
QY 420 aaaaaccgcagacactgcgaactcttgggtggcaggtacatacaattaatgtgcaga 479
    ||||| || || || || || || || || || || || || || || || || || || ||
DB 306 aaaaagccgcagagactgctgtcttggatgcccactgtcgaagatlaatagcacaga 365
    ||||| || || || || || || || || || || || || || || || || || || ||
QY 480 tgaatgcacatcatcttcaagaactttcccataccacccctccctcgtgattggatt 539
    ||||| || || || || || || || || || || || || || || || || || || ||
DB 366 tgaactggaattcatccagcaaatgatgtgcccatcccaattccctcgtgattggatt 425
    ||||| || || || || || || || || || || || || || || || || || || ||
QY 540 gcaatgcgaagaagcctgcgaacacatggtactatggagaatggaaactccttgatcca 599
    ||||| || || || || || || || || || || || || || || || || || || ||
DB 426 gtcaatgaagaagaacacatctactcgtcttggaagatgtaactccttgagcccca 485
    ||||| || || || || || || || || || || || || || || || || || || ||
QY 600 attccttaagaccaggggcttcttcttaacgcatatctcaagcaactggtacact 659
    ||||| || || || || || || || || || || || || || || || || || || ||
DB 486 ctgtcttaagaatcaagggagctgttcccgatgatacttcctcaggaacctgtgcataat 545
    ||||| || || || || || || || || || || || || || || || || || || ||
QY 660 tcaagaacgagctgtctgcgtgaaacatgcatctcaatgcatcagaatgagaa 719
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DB 546 tcaaaaggggaactgcttcttgctgaaacatgcatcttaactgcatcagatatagtcaca 605
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QY 720 gaagacaatcatctg 735
    ||||| || || || || || || || || || || || || || || || || || || ||
DB 606 gaagcgaaatcatctg 621
    ||||| || || || || || || || || || || || || || || || || || || ||
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## RESULT 13

AAH47112  
ID AAH47112 standard; cDNA: 1514 BP.

AC AAH47112;

XX 30-NOV-2001 (first entry)

XX O. cuniculus LOX-1 polypeptide encoding cDNA.

DE LOX-1; LDL; monoclonal antibody; low density lipoprotein; human;  
XX atherosclerosis; cardiovascular; kidney disease; inflammatory disorder;  
KM leukocyte; ss.  
XX Orxctolagus cuniculus.

OS Orxctolagus cuniculus.

XX

XX

XX

XX

XX

XX

XX

XX

XX

WO200164862-A1.

07-SEP-2001.

02-MAR-2001; 2001WO-JP01636.

PR 02-MAR-2000; 2000JP-0057745.  
PR 31-OCT-2000; 2000JP-0333116.  
XX  
XX (ABGE-) ABGENIX INC.  
XX

PI Kobayashi Y, Tsuji H, Kamada M, Sawamura T;

DR WPI; 2001-565503/63.

PT P-PSDB; AAB85871.

PT Human monoclonal antibodies recognizing oxidized low density

PT lipoprotein receptor for treatment of atherosclerosis and

XX cardiovascular and kidney diseases

XX Disclosure; Page 105-108; 131pp; Japanese.

CC The invention provides human monoclonal antibodies and their fragments  
CC binding to human oxidized low density lipoprotein (LDL) receptor (LOX-1),  
CC and inhibiting intracellular binding of the receptor to oxidized LDL.  
CC Drug compositions containing the Mab are useful in the treatment and  
CC prevention of atherosclerosis, cardiovascular and kidney diseases,  
CC inflammatory disorders and infiltration of leukocytes. The present  
CC sequence represents an O. cuniculus LOX-1 polypeptide encoding cDNA.

SQ Sequence 1514 BP; 414 A; 375 C; 322 G; 403 T; 0 other;

Query Match 37.3%; Score 277.6; DB 22; Length 1514;

Best Local Similarity 70.0%; Pred. No. 1, 2e-70;

Matches 389; Conservative 0; Mismatches 164; Indels 3; Gaps 1;

```
QY 183 agccctgcagagagctgcgaactcttcagaagagctcccaagagaactcaaggaagat 242
    ||||| || || || || || || || || || || || || || || || || || || ||
DB 299 agcccaagcagcagcagcagcagcttcccaagctcacaaaggaactcaagaatgat 358
    ||||| || || || || || || || || || || || || || || || || || || ||
QY 243 agacaccccttcagcttgaaagtgaaatccaaagacagagagctttacagaa 302
    ||||| || || || || || || || || || || || || || || || || || || ||
DB 359 agaaactctgcgaagagctgtgataaaatccaaagacaaatggaacttaacatca 418
    ||||| || || || || || || || || || || || || || || || || || || ||
QY 303 gaatcagaactccaaagacccctgcgaagagctgcgaacttcagctcgtccaca 362
    ||||| || || || || || || || || || || || || || || || || || || ||
DB 419 gtacctgaatctccaaagagctctgaaagaaatgaagaactttcagctcgtcccca 478
    ||||| || || || || || || || || || || || || || || || || || || ||
QY 363 agactgctctgcgcataaagaaactgtactctt--cactgggccccttgctggga 419
    ||||| || || || || || || || || || || || || || || || || || || ||
DB 479 agactgctctgcgcataaagaaactgtactcttctcctcgtgcatcttaattggga 538
    ||||| || || || || || || || || || || || || || || || || || || ||
QY 420 aaaaaccgcgacacccgcgaactcttgggtggcaggtacatacaattaatgtgcaga 479
    ||||| || || || || || || || || || || || || || || || || || || ||
DB 539 aagtagtcaagaagaatgctgtcttggaagcgcaggttcaaatcaagcacaga 598
    ||||| || || || || || || || || || || || || || || || || || || ||
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    ||||| || || || || || || || || || || || || || || || || || || ||
DB 599 agctcgggcttcatccagaagacgacttccatccagttccatccatccgagtgatt 658
    ||||| || || || || || || || || || || || || || || || || || || ||
QY 540 gcatcggaagaagcctgcgaacacatggtactatggaggaatggaactccttgattca 599
    ||||| || || || || || || || || || || || || || || || || || || ||
DB 659 gtctcggaagaaacccgactactacatgctcgttggaagacgttctcctcgtgccca 718
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QY 600 attccttaagaccaggggcttcttcttaacgcatatctcaagcaactggtacact 659
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QY 660 tcaagaacgagctgtctgcgtgaaacatgcatctcaatgcatcagacatagttcagaa 719
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DB 839 gaagcgaatcatctg 854
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```

## RESULT 14



CC identification and isolation of full-length cDNAs and genomic DNA  
 CC molecules which correspond to the SESTs. Proteins encoded by the SESTs  
 CC are useful in assays for determining biological activity and raising  
 CC antibodies. They may be useful for treatment of autoimmune disorders  
 CC (multiple sclerosis, insulin dependent diabetes), allergic conditions  
 CC (asthma), myeloid or lymphoid cell deficiencies, wounds, ulcers,  
 CC osteoporosis, osteoarthritis, central nervous system disorders  
 CC (Alzheimer's, Parkinson's, Huntington's disease, stroke), coagulation  
 CC disorders (haemophilia, thrombosis), inflammatory disorders (Crohn's  
 CC disease), tumours, bacterial, fungal or viral infections, depression and  
 CC psoriasis. AAA45926 to AAA45931 represent linker variants which are given  
 CC in the exemplification of the present invention.

xx  
 SQ Sequence 532 BP; 162 A; 132 C; 127 G; 111 T; 0 other:

Query Match 21.7%; Score 161.6; DB 21; Length 532;  
 Best Local Similarity 88.0%; Pred. No. 4.8e-37;  
 Matches 176; Conservative 0; Mismatches 24; Indels 0; Gaps 0;

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Db 333 aaacacttcacagaaatcaagaagaactgaaagaaagatagacacccctcacccaga 392

QY 122 agctgagcaggaataatcaagaagcagagagcttctgcagatgatcagaactccaag 181
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Db 393 agctgagcaggaataatcaagaagcagagagcttctgcagatgatcagaactccaag 452

QY 182 aagccctgcagagagctgcaactcttcagagaggtcccaagagaactcaaggaaaga 241
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 453 aagccctgcagagagctgcaactcttcagagaggtcccaagagaactcaaggaaaga 512

QY 242 tagaacacctcacttgaag 261
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Db 513 tagaacacctcactcctcgag 532
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Search completed: August 19, 2002, 22:01:22  
 Job time: 9047 sec



GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 19, 2002, 21:01:18 ; Search time 48.91 Seconds  
(without alignments)  
3736.482 Million cell updates/sec

Title: US-09-898-554-13  
Perfect score: 744  
Sequence: 1 atgactttgacgaagat.....caatcattgcaattag 744

Scoring table: IDENTITY\_NIC  
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database : Issued\_Patents\_NA:\*  
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2: /cgn2\_6/ptodata/1/ina/5B\_COMB.seq:\*  
3: /cgn2\_6/ptodata/1/ina/6A\_COMB.seq:\*  
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6: /cgn2\_6/ptodata/1/ina/backfillseq.seq:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
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6	287.2	38.6	1906	4	US-09-352-302-3
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8	72.4	9.7	990	2	US-09-113-788-2
9	61.2	8.2	528	3	US-08-772-440-7
10	61.2	8.2	2298	3	US-08-772-440-1
11	59.4	8.0	7218	1	US-08-232-463-14
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13	45.2	6.1	5661	3	US-08-938-105-2
14	41.8	5.6	340	1	US-08-182-175A-104
15	41.8	5.6	340	5	PCT-US92-06412-104
16	40	5.4	16442	3	US-08-781-891-208
17	39.2	5.3	1212	4	US-09-591-435-11
18	38.6	5.2	289	4	US-09-007-005-17
19	38.6	5.2	289	4	US-09-244-796-17
20	38.4	5.2	926	2	US-08-919-145-1
21	38.4	5.2	926	2	US-09-344-889-1
22	38	5.1	3489	2	US-08-728-323A-1
23	38	5.1	32207	2	US-08-770-379-20
24	38	5.1	32207	4	US-08-757-669A-20
25	38	5.1	32207	4	US-09-230-371A-20
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28	36.6	4.9	2680	2	US-08-742-923A-5
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31	36	4.8	533	6	5482709-5
32	36	4.8	543	6	5273901-6
33	35	4.7	1242	5	PCT-US93-03077-4
34	35	4.7	3279	5	PCT-US93-03077-2
35	33.8	4.5	4456	4	US-09-095-443-1
36	33.6	4.5	187	1	US-08-182-175A-90
37	33.6	4.5	187	1	US-08-474-633A-78
38	33.6	4.5	187	5	PCT-US92-06412-90
39	33.6	4.5	243	1	US-08-182-175A-56
40	33.6	4.5	243	1	US-08-474-633A-74
41	33.6	4.5	243	5	PCT-US92-06412-56
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43	33.6	4.5	1489	3	US-08-836-582-1
44	33.6	4.5	1489	4	US-09-265-566-1
45	33.4	4.5	486	3	US-08-493-071-13

## ALIGNMENTS

RESULT 1  
US-08-809-494A-5  
Sequence 5, Application US/08809494A  
Patent No. 5962260  
GENERAL INFORMATION:  
APPLICANT: Sawamura, Tatsuya  
TITLE OF INVENTION: Modified Low-Density Lipoprotein  
TITLE OF INVENTION: Receptor  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSSEE: McAlay Fisher Nissen Goldberg & Kiel  
STREET: 261 Madison Avenue  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10016-2391  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/809, 494A  
FILING DATE: 24-MAR-1997  
CLASSIFICATION: A35  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-321705  
FILING DATE: 30-NOV-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 7-214206  
FILING DATE: 31-JUL-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Goldberg, Jules E.  
REGISTRATION NUMBER: 24408  
REFERENCE/DOCKET NUMBER: JG-YY-4363PCT  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212 986-4090  
TELEFAX: 212 818-9479  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 1318 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: cDNA  
HYPOTHETICAL: NO  
ANTI-SENSE: NO  
ORIGINAL SOURCE:  
ORGANISM: Homo Sapiens

Sequence 5, Appli  
Sequence 3, Appli  
Sequence 3, Appli  
Patent No. 5482709  
Patent No. 5273901  
Sequence 4, Appli  
Sequence 2, Appli  
Sequence 1, Appli  
Sequence 90, Appli  
Sequence 78, Appli  
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Sequence 56, Appli  
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Sequence 1, Appli  
Sequence 13, Appli

TISSUE TYPE: Lung, placenta  
 IMMEDIATE SOURCE:  
 LIBRARY: Human lung cDNA  
 CLONE: lambdahlox-1  
 FEATURE:  
 NAME/KEY: 5'UTR  
 LOCATION: 66..125  
 FEATURE:  
 NAME/KEY: 3'UTR  
 LOCATION: 949..1309  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 127..948  
 US-08-809-494A-5

Query Match 40.1%; Score 298.2; DB 2; Length 1318;  
 Best Local Similarity 72.6%; Pred. No. 3.5e-83;  
 Matches 400; Conservative 0; Mismatches 148; Indels 3; Gaps 1;

QY 183 agccctcagagagctcgaactcttcagagaggtcccaagagaaactcaaggaaagat 242  
 DB 384 AGCCCGGCAACAGCAAGAAAGCTTCACAGAGTCAAGAAACGAACTCAAGAAATGAT 443  
 QY 243 agnaccctacccttgagctgaagcgaatccaaagacgaagagagcttcaagaa 302  
 DB 444 AGAAACCCCTTGCGAAGTGATGAAATCCAAAGCAATGGAACCTTCACCA 503  
 QY 303 gaatcagaacctcaaaagccctcgaagagagctcgaacttcaagctctgtccaca 362  
 DB 504 GAATCTGAATCTCCAAAGAACTGAGAGAGAGTAAATTTGTTCACTCTTCCGCA 563  
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RESULT 2  
 US-09-352-302-5  
 Sequence 5; Application US/09352302  
 Patent No. 6197937  
 GENERAL INFORMATION:  
 APPLICANT: Sawamura, Tatsuya  
 APPLICANT: Masaki, Tomoo  
 TITLE OF INVENTION: Modified Low-Density Lipoprotein  
 TITLE OF INVENTION: Receptor  
 NUMBER OF SEQUENCES: 8  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: McAnlay Fisher Nissen Goldberg & Kiel

STREET: 261 Madison Avenue  
 CITY: New York  
 STATE: NY  
 COUNTRY: USA  
 ZIP: 10016-2391  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/352,302  
 FILING DATE: 12-JUL-1999  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 6-321705  
 FILING DATE: 30-NOV-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 7-214206  
 FILING DATE: 31-JUL-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Goldberg, Jules E  
 REGISTRATION NUMBER: 24408  
 REFERENCE/DOCKET NUMBER: JG-YY-4363PCT/D  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 212 986-4090  
 TELEFAX: 212 818-9479  
 INFORMATION FOR SEQ ID NO: 5:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1318 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 HYPOTHEICAL: NO  
 ANTI-SENSE: NO  
 ORIGINAL SOURCE:  
 ORGANISM: Homo Sapiens  
 TISSUE TYPE: Lung, placenta  
 IMMEDIATE SOURCE:  
 LIBRARY: Human lung cDNA  
 CLONE: lambdahlox-1  
 FEATURE:  
 NAME/KEY: 5'UTR  
 LOCATION: 66..125  
 FEATURE:  
 NAME/KEY: 3'UTR  
 LOCATION: 949..1309  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 127..948  
 US-09-352-302-5

Query Match 40.1%; Score 298.2; DB 4; Length 1318;  
 Best Local Similarity 72.6%; Pred. No. 3.5e-83;  
 Matches 400; Conservative 0; Mismatches 148; Indels 3; Gaps 1;

QY 183 agccctcagagagctcgaactcttcagagaggtcccaagagaaactcaaggaaagat 242  
 DB 384 AGCCCGGCAACAGCAAGAAAGCTTCACAGAGTCAAGAAACGAACTCAAGAAATGAT 443  
 QY 243 agnaccctacccttgagctgaagcgaatccaaagacgaagagagcttcaagaa 302  
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Sequence 1, Application US/09352302
Patent No. 6197937

GENERAL INFORMATION:
APPLICANT: Sawamura, Tatsuya
APPLICANT: Masaki, Tomoo
TITLE OF INVENTION: Modified Low-Density Lipoprotein
TITLE OF INVENTION: Receptor
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: McAlay Fisher Nissen Goldberg & Kiel
STREET: 261 Madison Avenue
CITY: New York
STATE: NY
COUNTRY: USA
ZIP: 10016-2391

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/352,302
FILING DATE: 12-JUL-1999
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-321705
FILING DATE: 30-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-214206
FILING DATE: 31-JUL-1995
ATTORNEY/AGENT INFORMATION:
NAME: Goldberg, Jules E
REGISTRATION NUMBER: 24408
REFERENCE/DOCKET NUMBER: JG-YY-4363PCT/D
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 986-4090
TELEFAX: 212 818-9479
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1897 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Bos taurus
TISSUE TYPE: Vascular endothelial cells
IMMEDIATE SOURCE:
LIBRARY: Bovine aortic endothelial cell cDNA
CLONE: pBLOX-1
FEATURE:
NAME/KEY: polyA_site
LOCATION: 1880..1897
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NAME/KEY: misc_RNA
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OTHER INFORMATION: /function="PolyA Signal"
FEATURE:
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LOCATION: 1..34
FEATURE:
NAME/KEY: 3'UTR
LOCATION: 848..1897
FEATURE:
NAME/KEY: CDS
LOCATION: 35..847
US-09-352-302-1

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[illegible]

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: APPLICATION NUMBER: JP 7-214206
: FILING DATE: 31-JUL-1995
: ATTORNEY/AGENT INFORMATION:
: NAME: Goldberg, Jules E
: REGISTRATION NUMBER: 24408
: REFERENCE/DOCKET NUMBER: JG-YY-4363PCT
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 212 986-4090
: TELEFAX: 212 818-9479
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1906 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: HYPOTHEICAL: NO
: ANTI-SENSE: NO
: ORIGINAL SOURCE:
: ORGANISM: Bos taurus
: TISSUE TYPE: Vascular endothelial cells
: IMMEDIATE SOURCE:
: LIBRARY: Bovine aortic endothelial cells cDNA
: CLONE: pBLOX-1
: FEATURE:
: NAME/KEY: polyA_site
: LOCATION: 1889..1906
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: FEATURE:
: NAME/KEY: 5'UTR
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: NAME/KEY: CDS
: LOCATION: 35..856
: US-08-809-494A-3

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 Best Local Similarity 71.0%; Pred. No. 1.1e-79;  
 Matches 395; Conservative 0; Mismatches 158; Indels 3; Gaps 1;

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OY 243 agacccctcagctgaagctgaagaaatccaaagagcagggaggctcttcagaa 302
Db 349 AGAAACCCCTTGCCACAGCTGTGATGAGAAATCAAGAACTTAATGGAATCTACCGCA 408
OY 303 gaatcagaacctccaagaagccctgcgaagagctgcaactcttcagctcttcacaa 362
Db 409 GAACCTGATCTCCAAGAGTTCTGAAGAGCAGCAAACTATTCAGAGCTTGTGCCCA 468
OY 363 agactggtctggcgtataaagaactgttac--tcttcagtggcccttggctggga 419
Db 469 AGACTGGCTCTGGCATGAGAAAGAACTGTTACCAATTTCTGCTGCTTTTAATGGGA 528
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OY 480 tgatctgacatcatcttaacaagaattcccatcacacctcccatcttgatgtgatt 539
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OY 720 gaagacaataacttg 735
Db 829 GAAGCGAATCTATTG 844

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RESULT 6  
 US-09-352-302-3  
 Sequence 3, Application US/09352302  
 Patent No. 6197937  
 GENERAL INFORMATION:  
 APPLICANT: Sawamura, Tatsuya  
 TITLE OF INVENTION: Modified Low-Density Lipoprotein  
 NUMBER OF SEQUENCES: 8  
 CORRESPONDENCE ADDRESS:  
 STREET: McAlay Fisher Nissen Goldberg & Kiel  
 CITY: New York  
 STATE: NY  
 COUNTRY: USA  
 ZIP: 10016-2391  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/352,302  
 FILING DATE: 12-JUL-1999  
 CLASSIFICATION:  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 6-321705  
 FILING DATE: 30-NOV-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 7-214206  
 FILING DATE: 31-JUL-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Goldberg, Jules E  
 REGISTRATION NUMBER: 24408  
 REFERENCE/DOCKET NUMBER: JG-YY-4363PCT/D  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 212 986-4090  
 TELEFAX: 212 818-9479  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 1906 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 HYPOTHEICAL: NO  
 ANTI-SENSE: NO  
 ORIGINAL SOURCE:  
 ORGANISM: Bos taurus  
 TISSUE TYPE: Vascular endothelial cells  
 IMMEDIATE SOURCE:  
 LIBRARY: Bovine aortic endothelial cells cDNA  
 CLONE: pBLOX-1  
 FEATURE:  
 NAME/KEY: polyA\_site  
 LOCATION: 1889..1906  
 FEATURE:

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; NAME/KEY: misc_RNA
; LOCATION: 1864...1873
; OTHER INFORMATION: /function="Polya signal"
; FEATURE:
; NAME/KEY: 5'UTR
; LOCATION: 1...34
; FEATURE:
; NAME/KEY: 3'UTR
; LOCATION: 857...1906
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 35..856
; US-09-352-302-3

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Query Match          38.6%; Score 287.2; DB 4; Length 1906;
Best Local Similarity 71.0%; Pred. No. 1,1e-79;
Matches 395; Conservative 0; Mismatches 158; Indels 3; Gaps 1;

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QY 183 agccctgcagagagctgcaaacctcttcagagagagctcccaagagaaactcaaggagaaat 242
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DB 349 AGAAACCCCTGCCACAGCTGATGAGAAATCCAGAACTAATGGAACCTTCACGCCCA 408
QY 303 gaatcagaacctcaagaagccctgcagaagagctgcaaaccttccagctctgcagaca 362
DB 409 GAACCTCAATCTCCAGAAATTTCTGAAGAAGGCGAGCAAACTATTACAGTCTTCCCA 468
QY 363 agactgctctgycataaagaactgttaccc--tctccatgagcccttggctggga 419
DB 469 AGACTGCTCTGCGATGAAGAAACTGTACCAATTTCTCTGCGCTTTTAAATGGGA 528
QY 420 aaaaaacgcgcagacctgccaactcttgggtgcccagttactacaattatggtcaga 479
DB 529 AAAAAGCAGAGAAACGCTTGTCTTGGATGCCCACTTCTGAAGTTAATACACAGA 588
QY 480 tgcattacatcatcttacaagaacttcccataccctcccatcttcgagatgatt 539
DB 589 TGAACCTGGAATTCATCCAGAAATGATTGCCCATTTCCCTTCGAGAGGGGTT 648
QY 540 gcatcggaagaagcctgycacaacatggtctatggagaaatggaactccttgaattca 599
DB 649 GTCAAATGAGAAACCAATTAATCTGCTGCTTGGAGAGATGCTCTTGAAGGCCCA 708
QY 600 attcttaagacagagggcgcttcttaccagctatattcaagcaactgtagatcc 659
DB 709 CTGTGTTAGAAATTCAGGAGCTGTTTCCGATGATCTTCAGGAGCTGTGATATAT 768
QY 660 tcaagacgagacgtgtctgctgaaactcatctaatgcaatcagcagcagcagaa 719
DB 769 TCAAGGGAACGTGTTTCTGAAACCTGATTTAAACGCAATTAATGATATGCTCAAA 828
QY 720 gaagacaatcattg 735
DB 829 GAAGGCAATCTATTTG 844

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RESULT 7
US-08-688-342-2
; Sequence 2, Application US/08688342
; Patent No. 5871964
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Goll, Surya K.
; APPLICANT: Hillman, Jennifer L.
; TITLE OF INVENTION: NOVEL HUMAN C-TYPE LECTIN
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.

```

```

; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: US
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq Version 1.5
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/688,342
; FILING DATE: Filed Herewith
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0095-1 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; INFORMATION FOR SEO ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 990 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; IMMEDIATE SOURCE:
; LIBRARY: MMLR1D701
; CLONE: 515847
; US-08-688-342-2

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Query Match          9.7%; Score 72.4; DB 2; Length 990;
Best Local Similarity 52.8%; Pred. No. 5,7e-13;
Matches 204; Conservative 0; Mismatches 176; Indels 6; Gaps 2;

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QY 344 ttcaagtccttgcacacaagactgctcgcataaagaanaactgttactcttccatg 403
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QY 404 ggcctt---tgcttgagaaanaacccgcagactgccaactcttgggtgcccagttac 460
DB 343 TGTCATTAATCTCTGAGGATGAAGTAAGACAACTGCGCAACTGCGCTTAATCTCC 402
QY 461 tacaattatgctgagatgacatcattcctt---acaagcaattcccatacca 517
DB 403 TAAAGATAGACGCTCAAAATGAATTTGGATTTAATGAAGAAAGATGCTTCCAACTG 462
QY 518 cctcccatcttgatgattgcatcgcgaagaagcctgcccacaacatggtctatggaga 577
DB 463 ATAATTAATTTGGATAGCGCTTTCGCGCCAGACTGAGTACATGCTCTGCGAGG 522
QY 578 atggaactccttgaatttcaattcatttaagaccagggcgcttcttcaagtatat 637
DB 523 ATGATCAACATCTCTTCTTAATTAATTCAGATCAGAACACAGCTACCAAGAAACC 582
QY 638 catcaagcaactgctgcatccttcaagaagcgtgtctgcgtgaaactgcatctaa 697
DB 583 CATCTCCAATTTGATGATGATTCACGTGCAGTCATTTATGACCAACTGTGATGTGC 642
QY 698 ttgcatcagcatatgctcagaagaag 723
DB 643 CCTCATATAGTATTTGTGAGAGAGAG 668

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RESULT 8
US-09-113-788-2
; Sequence 2, Application US/09113788
; Patent No. 5969104
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice
; APPLICANT: Cocks, Benjamin G.

```

Matches	204;	Conservative	0;	Mismatches	176;	Indels	6;	Gaps	2;
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RESULT 12  
US-08-772-440-9  
; Sequence 9, Application US/08772440  
; Patent No. 6046158  
; GENERAL INFORMATION:  
; APPLICANT: Arizumi, Kiyoshi  
; APPLICANT: Takashima, Akira  
; TITLE OF INVENTION: UNIQUE DENDRITIC CELL-ASSOCIATED C-TYPE  
; TITLE OF INVENTION: LECTINS, DECTIN-1 AND DECTIN-2; COMPOSITIONS AND USES  
; TITLE OF INVENTION: THEREOF  
; NUMBER OF SEQUENCES: 42  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P.O. Box 4433  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: USA  
; ZIP: 77210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: PatentIn Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/772,440  
; FILING DATE: CONCURRENTLY HERewith  
; CLASSIFICATION: 433  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Parker, David L.  
; REGISTRATION NUMBER: 32,165  
; REFERENCE/DOCKET NUMBER: UTXD.493  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 512/418-3000  
; TELEFAX: 512/474-7577

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RESULT 13
US-08-938-105-2
Sequence 2, Application US/08938105
Patent No. 635151
GENERAL INFORMATION:
APPLICANT: leinwand, Leslie A.
APPLICANT: Vikstrom, Karen L.
TITLE OF INVENTION: TRANSGENIC MODEL FOR HEART FAILURE
NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross P.C.
STREET: 1700 Lincoln St., Suite 3500
CITY: Denver
STATE: CO
COUNTRY: U.S.A.
ZIP: 80203
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/938,105
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Crook, Wannell M.
REGISTRATION NUMBER: 31,071
REFERENCE/DOCKET NUMBER: 3595-4
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEO ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 5661 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..5661
US-08-938-105-2

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REFERENCE/DOCKET NUMBER: BB-1031  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (302) 992-4929  
TELEFAX: (302) 892-7949  
TELEX: 835420  
INFORMATION FOR SEQ ID NO: 104:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 340 base pairs  
TYPE: NUCLEIC ACID  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
ORIGINAL SOURCE:  
STRAIN: E. coli  
CELL TYPE: DH5 alpha  
IMMEDIATE SOURCE:  
CLONE: segment 534 [seg 534]  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 3..326  
OTHER INFORMATION: /function= "synthetic seed storage protein"  
OTHER INFORMATION: /product= "protein"  
OTHER INFORMATION: /gene= "ssp"  
OTHER INFORMATION: /standard\_name= "SSP-534"  
PCT-US92-06412-104

Query Match 5.6%; Score 41.8; DB 5; Length 340;  
Best Local Similarity 47.5%; Pred. No. 0.0011;  
Matches 124; Conservative 0; Mismatches 137; Indels 0; Gaps 0;  
QY 60 caagaagcctaagaagaggtccagagagaactcaagggaagatlagaccaccgccg 119  
DB 2 CATGAGAGAGAGATGAAAAAGCTCAAGAGAGAAATGCTTAAGATGAAGAAGCAAAATGTG 61  
QY 120 gaagctgagcagaatcccaagagcagagagcttctcagatgaltcagaactcca 179  
DB 62 GAAACTGAAGAGAGAAATGAAGAGCTCGAAGAGAGATGAAGATCATGAGAGAGAGAT 121  
QY 180 agaagccctgagagagctgcaactcttcagagaggtcccaagagagaactcaaggaaa 239  
DB 122 GAAAAAGCTGGAAGAAAAAGATGAAGCTATGAGAGACAAAGATGAATGCTTGAGAGAAA 181  
QY 240 gatagacacccctcaacttgaagctgaacgagaatccaaagacagagagagcttctaca 299  
DB 182 GATGAAGAAGCTCGAAGAGAGATGAAGTCAATGAGAGAGAGATGAATGAAGCTCGAAGA 241  
QY 300 gaagaatcagaactccaaga 320  
DB 242 AAAGATGAAGCAATGAGAGA 262

Search completed: August 19, 2002, 22:02:32  
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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: August 19, 2002, 19:03:05 ; Search time 1710.4 Seconds  
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5870.986 Million cell updates/sec

Title: US-09-898-554-13

Perfect score: 744

Sequence: 1 atgaccttgcagacaagat.....caatcattgcaaatgtag 744

Scoring table: IDENTITY\_NUC

Searched: 13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database :

EST.\*  
1: em\_estdb.\*  
2: em\_esthum.\*  
3: em\_estlin.\*  
4: em\_estnu.\*  
5: em\_estov.\*  
6: em\_estpl.\*  
7: em\_estlo.\*  
8: em\_hlc.\*  
9: gb\_estl.\*  
10: gb\_est2.\*  
11: gb\_hlc.\*  
12: gb\_gss.\*  
13: em\_gss\_hum.\*  
14: em\_gss\_inv.\*  
15: em\_gss\_pln.\*  
16: em\_gss\_vrt.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	297.8	40.0	851	9 AUI35631	AUI35631 AUI35631
2	285.4	38.4	900	9 AL546824	AL546824 AL546824
3	265.6	35.7	827	10 B1522607	B1522607 603175620
4	244.8	32.9	514	9 A1243883	A1243883 qh78a08.x
5	241.4	32.4	499	10 BG383949	BG383949 302408.MA
6	199.4	26.8	426	9 AA682386	AA682386 zj86b12.s
7	197.6	26.6	718	9 AUI38854	AUI38854 AUI38854
8	197.6	26.6	760	9 AUI37679	AUI37679 AUI37679
9	177.2	23.8	731	9 AUI35523	AUI35523 AUI35523
10	171.6	23.1	746	10 BG547497	BG547497 602574930
11	171.6	22.7	934	9 AL551100	AL551100 AL551100
12	168.8	22.1	910	10 B1601086	B1601086 603249577
13	153.4	20.6	526	10 B1289895	B1289895 UR-R-DK0-
14	140	18.8	472	10 R62556	R62556 y11b10.r1
15	132.6	17.8	378	10 R07930	R07930 yf16e04.r1
16	116.4	15.6	480	10 B1541952	B1541952 456045.MA
17	111	14.9	780	10 BG573639	BG573639 602594660

C	18	92.4	12.4	407	10	BF934257	BF934257 IL5-MT027
C	19	82.8	11.1	258	10	BF895809	BF895809 IL2-MT017
C	20	77.8	10.5	277	9	AA620341	AA620341 af07a11.s
C	21	74.4	10.0	659	10	B1018962	B1018962 IL3-MT026
C	22	73	9.8	356	9	BB868965	BB868965 BB868965
C	23	73	9.8	363	9	BB869276	BB869276 BB869276
C	24	68.2	9.2	253	9	BB564191	BB564191 BB564191
C	25	66	8.9	320	9	BE175194	BE175194 OV2-HT057
C	26	65	8.9	673	9	AV721179	AV721179 AV721179
C	27	63	8.5	940	10	BF982378	BF982378 60230808
C	28	49	6.6	647	10	BF301405	BF301405 602029862
C	29	48.4	6.5	258	10	BF895809	BF895809 IL2-MT017
C	30	47.6	6.4	650	9	BB618338	BB618338 BB618338
C	31	45.8	6.2	644	12	ACS33202	ACS33202 IM0060M04
C	32	45.8	6.2	1159	12	CNS015XR	AL106041 Drosophila
C	33	45.6	6.1	294	10	BE767906	BE767906 QV1-GN006
C	34	45.4	6.1	1731	11	AK006127	AK006127 Mus muscu
C	35	45.2	6.1	567	10	BG793253	BG793253 U7SM-SM10
C	36	45.2	6.1	634	12	AZ008814	AZ008814 RPCI-23-3
C	37	44.8	6.0	486	10	BF839762	BF839762 RC3-HM010
C	38	44.8	6.0	637	10	BE395825	BE395825 601310060
C	39	44.8	6.0	865	10	BG824296	BG824296 602727315
C	40	44.8	6.0	913	10	BG120501	BG120501 602346818
C	41	44.8	6.0	1044	10	BE795516	BE795516 601590192
C	42	44.8	6.0	1123	10	BG325379	BG325379 602424064
C	43	44.6	6.0	636	10	BF127555	BF127555 601810204
C	44	44	5.9	676	10	BM095514	BM095514 fv31901.y
C	45	44	5.9	750	10	BG120527	BG120527 602346849

#### ALIGNMENTS

RESULT 1  
LOCUS AUI35631 851 bp mRNA linear EST 24-OCT-2000  
DEFINITION AUI35631 PLACE1 Homo sapiens CDNA clone PLACE1002536 5', mRNA  
ACCESSION AUI35631  
VERSION AUI35631.1 GI:10996170  
KEYWORDS EST.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE 1 (bases 1 to 851)  
Ota, T., Nishikawa, T., Suzuki, Y., Ishii, S., Saito, K., Kawai, Y.,  
Yamamoto, J., Wakamatsu, A., Nakamura, Y., Nagai, T., Sugano, S. and  
Isogai, T.  
HRI human CDNA project  
Unpublished (2000)  
CONTACT: Takao Isogai  
Genomics Laboratory  
Helix Research Institute  
1532-3 Yana, Kisarazu, Chiba 292-0812, Japan  
Tel: 81-438-52-3951  
Fax: 81-438-52-3952  
Email: genomesehri.co.jp  
HRI human CDNA project; 5'- & 3'-end one pass sequencing; Helix  
Research Institute; CDNA library construction; Department of  
Virology, Institute of Medical Science, University of Tokyo, and  
Helix Research Institute.

FEATURES  
source  
location/Qualifiers  
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/tissue\_type="placenta"  
/note="Vector: pMT85FL3"

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Oy 495 ctacaagaacatctccatataccacccctcccatcttgatctgattgcatcgaagaagcc 554
Db 270 CCAAGCAAGCAATTTCCACAGCTTTCATCTTGATGGGCTGTCTGGAGAAACC 211
Oy 555 tggcaacatggtcgtatggagaatggaactccttgaaattcgaattccttaagaccag 614
Db 210 CAGCTACCCCTATGGCTCTGGAGAGACGGTTCCTTGATGCCCTACTTATTTAGAGTCCG 151
Oy 615 gggcgtctcttcaagctatcatatcatcaagaactgtgcatcctcaactcaagaagagctgt 674
Db 150 AGCGCTGTCTCCACAGATACCTTTCAGTACTGTGCAATATATACAGAGAGAGCTGT 91
Oy 675 gtctctgaaactgcatctaaattgcatcgaacatgcatcgaagaagaacaatc 730
Db 90 TTATGGGAAAACTGCATTTTACCTGCTTCAGTATATATGACAGAGAGCAAAACC 35

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BG383949 499 bp mRNA linear EST 12-MAR-2001
LOCUS 302408 MARC 1PIG Sus scrofa CDNA 5', mRNA sequence.
DEFINITION BG383949
ACCESSION BG383949.1 GI:13308421
VERSION BG383949.1 GI:13308421
KEYWORDS EST.
SOURCE pig.
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suidae; Suidae; Sus.
1 (bases 1 to 499)
Fahnenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E.,
Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W.,
and Keele,J.W.
Design and use of two pooled tissue normalized CDNA libraries for
EST discovery in swine
Unpublished (2000)
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smithemail.marc.usda.gov
Single pass sequencing. Bases called and alt-trimmed with phred
v0.980904.e. Vector identified by cross-match with the -minscore 18
and -mismatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTTCCAGTCACGACG
Plate: 89 Row: B Column: 13
Seq primer: ATTTAGTGACACTATAG.
Location/Qualifiers
1. 499
/organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_lib="MARC 1PIG"
/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: PCMV SPORT6; Site.1: XbaI; Site.2: XhoI;
library made from pooled tissue from day 11, 13, 15, 20,
and 30 embryos."
BASE COUNT 146 a 123 c 114 g 116 t
ORIGIN
Query Match 32.4%; Score 241.4; DB 10; Length 499;
Best Local Similarity 71.3%; Pred.No.1.1e-54;
Matches 333; Conservative 0; Mismatches 131; Indels 3; Gaps 1;
Oy 199 gcaaaccttcagaagaccagagagaactcaagggaagaatagacaccctcacttg 258
Db 33 GAAAAATCTTCCAGAGTCACAAAGGAAGAACTGATAGAACTTTGGCCAC 92

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Oy 259 aagctgaacgagaatccaaagagcagagagctcttacaagaatcagaactcaca 318
Db 93 AAATTGGATGAAAAATCCAGAAACCTGATGAGCTTCACAGCAGAACTGGAATCTTCA 152
Oy 319 gaagcccttgcaagaagctgcaaatcttcaggtccttgctccaaagagctgctgcat 378
Db 153 AAAGCTTGAGAAAGAGGGGAAACTTTTCAGGTCCTTGTCCCAAGACTGGCTGTGCAT 212
Oy 379 aaagaacagcttaac---cccttcaatgggccccttgctgggaaaaaacggcaacc 435
Db 213 GAAGAAACCTGTATCAAAATTTCTCTGCGCCATTTAGTTGGGAAAAAACCGGAGAAC 272
Oy 436 tggcaatcttgggtggccagttactaacaataatggtgcagatgcatgcatc 495
Db 273 TGCTTGTCTTTGGATGGCCCAACTGCTGAAGATTAATATGACAGACAGATCTGGAATTCATC 332
Oy 496 ttacaagaacttccatccacccctccatcttgatgtgatgtgcatcggagaagcct 555
Db 333 CAGCAAAACCATGCCCATTCATTTCCATTCGTGATGGGGTTATCTGTGAGGAAACC 392
Oy 556 ggcacaacatggcctaigggagaatggaactccttgaaattcgaatccttaagaccag 615
Db 393 AACAACTCATGGCTCTGGAGAGAGGATCTTCTTGATGCCCACTGTTAGACTTCAG 452
Oy 616 ggcgtctcttacaagctatcatcaagaactgtgcatcctca 662
Db 453 GGAGCTGCTTCCCAATGATGTATCTTCAGGCACCTGTGCTGATATACA 499

RESULT 6
AA682386/c 426 bp mRNA linear EST 19-DEC-1997
LOCUS z186b12.s1 Soares_fetal_liver_spleen_INFIS_S1 Homo sapiens CDNA
DEFINITION clone IMAGE:461759.3' similar to SW:MKGD_HUMAN P26718 MKG2-D TYPE
II INTERMEMBRANE PROTEIN. ; mRNA sequence.
ACCESSION AA682386
VERSION AA682386.1 GI:2669667
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 426)
Hillier,L., Allen,M., Bowles,L., Dubuque,T., Geisler,G., Jost,S.,
Krizman,D., Kucaba,T., Lacy,M., Le,N., Lennon,G., Marra,M., Martin
,J., Moore,B., Schellenberg,K., Stepien,M., Tan,F., Theisling,B.,
White,Y., Wylie,T., Waterston,R. and Wilson,R.
WashU-NCI human EST Project
Unpublished (1997)
Contact: Wilson RK
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@wustl.wustl.edu
This clone is available royalty-free through LNW ; contact the
IMAGE Consortium (info@image.lnl.gov) for further information.
Possible reversed clone: similarity on wrong strand
Seq primer: -40m3 fwd. ET from Amersham
High quality sequence stop: 381.
Location/Qualifiers
1. 426
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="IMAGE:461759"
/clone_lib="Soares_fetal_liver_spleen_INFIS_S1"
/sex="male"
/dev_stage="20 week-post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: Liver and Spleen; Vector: pRT3D (Pharmacia)
with a modified polylinker; Site.1: Pac I; Site.2: Eco RI;
this is a subtracted version of the original Soares fetal

```



1532-3 Yana, Kisarazu, Chiba 292-0812, Japan  
Tel.: 81-438-52-3951  
Fax: 81-438-52-3952  
Email: genomics@hri.co.jp  
HRI human cDNA project; 5' - & 3' - end one pass sequencing; Helix Research Institute; cDNA library construction; Department of Virology, Institute of Medical Science, University of Tokyo,<sup>1</sup> and

Email: [genomacse@ri.co.jp](mailto:genomacse@ri.co.jp)  
 HRI human cDNA project: 5' - 3' end one pass sequencing: Helix  
 Research Institute, cDNA library construction: Department of  
 Virology, Institute of Medical Science, University of Tokyo, and  
 Helix Research Institute.  
 Location/Qualifiers  
 1..760

BASE COUNT	221 a	171 c	174 g	191 t	3 others
BRIGIN					
	/organism="Homo sapiens"				
	/db_xref="taxon:9606"				
	/clone="PLACEI006968"				
	/clone_id="PLACEI"				
	/tissue_type="placenta"				
	/note="vector: pME185FL3"				

Query Match:	26.68%	Score 197.6:	DB 9,	Length 760;
Best Local Similarity:	73.48%	Pred. No. 9e-43:		
Matches 292, Conservative	0,	Mismatches 101,	Indels 5,	Gaps 3;

QY	183	agccctcagagagctctgcaaaactcttcagagagctcccgagagaaactcaagggaagat	242
Db	313	AGCCCGGCACACAGAGAGAAGAGCTTCCACAGAGATCAGAAAAAGAACTCAAGGAATGAT	372
QY	243	agacacccctcaccttgaagctctgaacgagagaaatccaaagagcagagagacttctcacaga	302
Db	373	AGAAACCTTGCTCGGAGAGCTGATGAGAAATCCAAAGAGCAAAATGGAACTTCACACACA	432
QY	303	gaatcagaagactccaagaagccctgcagaagagctgcaaaactttagctctgtccaca	362
Db	433	GAATTCGATCTCCACAAAGAACACTGAAAGAGATACCAAAATTTGACGCTCCTTGCCGGA	492
QY	363	agactgagctctgcagctaaagaaactgttaactctctt---caatggcgcccttggttgga	419
Db	493	AGACTGGATCTGCGCATGGAGAAACCTGTTACCTATTTTCTCGGGCTCATTTAACTGGGA	552
QY	420	aaaaaacccgagacagacttgcacaaactcttggctgggtgcagcttactacaaatlaatgctgcaga	479
Db	553	AAAGAGCCACAGAGAGTGCTGTTGTTGGATGCCAAGTTCGTGAAATTAATAGCAGAC	612
QY	480	tgatctgcacatcatcttaacaaagaattcccatacc-aaactcccattctgatttgat	538
Db	613	TGATCTGCACCTTCATCCAGCAGCAAGCAATTTCCATTCCCAAGTTTTCATCTTGATGGGGGC	672
QY	539	tg-catcggaagaagcctgcgcacaccactgctatggga	575
Db	673	TGCTCTCGGAGGAANCCAGATTCCCATAGGCTCTTGGA	710

RESULT	9
AU135523	
LOCUS	
DEFINITION	AU135523 731 bp mRNA linear EST 24-OCT-2000
ACCESSION	AU135523 PLACE1 Homo sapiens cDNA clone PLACE1002267 5', mRNA sequence.
VERSION	AU135523
KEYWORDS	AU135523.1 GI:1096062
SOURCE	EST.
ORGANISM	human.
REFERENCE	Homo sapiens
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 731) Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y., Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and Isogai,T. HRI human cDNA project Unpublished (2000)
TITLE	Contact: Takao Isogai
JOURNAL	Genomics Laboratory
COMMENT	Helix Research Institute 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan Tel: 81-438-52-3951 Fax: 81-438-52-3952 Email: genom@cs.hri.co.jp HRI human cDNA project; 5'- & 3'-end one pass sequencing; Helix Research Institute; cDNA library construction; Department of Virology, Institute of Medical Science, University of Tokyo, and Helix Research Institute.  Location/Qualifiers
FEATURES	

```

source
1..731
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="PLACE1002867"
/clone_1b="PLACE1"
/tissue_type="placenta"
/vector="pME185FL3"

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Query Match	23.8%	Score 177.2	DB 9,	Length 731,
Best Local Similarity	74.0%	Pred. No. 3e-37,		
Matches 251; Conservative	0;	Mismatches 84;	Indels 4;	Gaps 2

OY	183	agcccttcaggagactgtcgaacctcttccaagagagtcgccgaaagaagactcaagggaaaagt	242
Db	313	AGCCCGGCACACAGAAGAAAGCTTTCACAGSAGTCAGAAAACGAATCAAGAAATGAT	372
OY	243	agacaccctcacccitgaagcttgacgcagagaatctcaagaagcagagagctctacaaga	302
Db	373	AGAAACCCCTTGCTCGGAAGCTGGAATAAGAGAAATCCAAAGAGCAAATGGAACTTCCACCACA	432
OY	303	gaatcagaacctccaagaagccctgcagaagctcgaaactcttcaagcttcgtgccaca	362
Db	433	GAACTGTGAATCTCCAAGAAGACCTGACAGAGACTAGCAAAATTGTTCAGCTCCTTTGCCGA	492
OY	363	agact- gactctgtgcataaagaanaactgttaectctt---ccatgycgccctttgcttgg	418
Db	493	AGACGTGGATCTGGCATGAGAAAACTGTATTACTTAATTTTCCTCGGGCTCATTTAATCTGG	552
OY	419	aaaaaaacccgcagagaccttgcacactcttggctggcgacttactacaanaatltaatgltgcag	478
Db	553	AAAAAGCCCAAGAGAAAGTGCTGCTCTTTGGAGCCCAAGTGTCTGAAAATTAATATAGCACAG	612
OY	479	atgatctgacattcatcttacaagaanaattccccatccae	517
Db	613	CTGATCTGGACTTCAATCCACACAGCAATTTCTTCAATMCCA	651

```

RESULT 10
BG547497
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

```

```

BG547497          746 bp      mRNA      linear      EST 04-APR-2001
602574930F1 NIH_MGC_77 Homo sapiens cDNA clone IMAGE:4702998 5',
mRNA sequence.
BG547497
BG547497.1  GI:13546162
EST .
human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 746)
1 (Bases 1 to 746)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: CLOnTECH Laboratories, Inc.
cDNA Library Preparation: CLOnTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)
DNA sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LMNL at:
http://Image.lmnl.gov
Plate: LCM1540 row: 1 column: 07
High quality sequence stop: 741.
Location/Qualifiers
1..746
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4702998"
/clone_lib="NIH_MGC_77"

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us-09-898-554-13.rst

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1. 934
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CSOD1066rpl4"
/clone_lib="LFI_NFL006_PL2"
/tissue_type="placenta"
/notes="Vector: pCMVSPORT 6, Site_1: NotI; 1st strand cDNA
was primed with a NotI-oligo(dT) primer. Five prime end
enriched, double-stranded cDNA was digested with NotI and
cloned into the NotI and EcoRV sites of the pCMVSPORT 6
vector. Library was normalized. Library was constructed by

```

Life Technologies. Contact : Feng Liang Life Technology  
a division of Invitrogen 9800 Medical Center Drive

BASE COUNT	ORIGIN
285	a
196	c
214	g
237	t
2	others

Query Match	23.1%	Score 171.6	DB 9	Length 934
Best Local Similarity	74.4%	Pred. No. 1.1e-35		
Matches 229	Conservative 1	Mismatches 75	Indels 3	Gaps 1
Qy 183	agccctgcagagagctgcgtaaacctctcagagagctccacagagagactcaaggaagat	242		
Db 288	AGCCCGGCAACAGAGAGAGAAAGCTTCCACAGSAGTCAGAAAAAGAACTCAAGGAATGAT	347		
Qy 243	agacaacctcaacctgtaagctgcgacgagaatccaaagaagcagagagactctacagaa	302		
Db 348	AGAMACCTTCTCTCGAAGCTGTAAGAGAAATCCAAAGAGCAAAATGGAACTTCACACCA	407		
Qy 303	gaatcagaacctccaaagaagccctgcagaaagctcgaactcttcagctctgtccaca	362		
Db 408	GAATCTGAATCTCCCAAGAAACACTGAAGAGATAGCAAAATTCTTACGCTCTTGTCGGA	467		
Qy 363	agactgctctgcgacaaagaanaactgttacctctt--ccatgggcctcttgctggaga	419		
Db 468	AGACTGATCTGTGCGATGAGAAACTGTACTATTTCCTGGGCTCATTTAACTGGGA	527		
Qy 420	aaaaaacccgcagagactcgcactcttctgggtggtgccagttactacaatatgaatgggcaga	479		
Db 528	AAAGGCGCAAGAGAGTCTTGCTTTGGATGCCAAGTTGCGAAATTAATAGCACAGC	587		
Qy 480	tgatctga 487			
Db 588	TGATCTGA 595			

DEFINITION	ACCESSION	VERSION	KEYWORDS	SOURCE	ORGANISM	REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
603249577.F1 NIH_MGC_96 Homo sapiens cDNA clone IMAGE:5301234 5'	mRNA sequence.	B1601086	B1601086.1 GI:15494025 EST.	human.	Homo sapiens	Eukaryotes; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.	NIH-MGC	<a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> . 1 (bases 1 to 910)	National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)	Contact: Robert Strausberg, Ph.D. Email: scapabs@email.nih.gov Tissue Procurement: Miklos Palcovits, M.D., Ph.D. CDNA Library Preparation: Michael J. Brownstein (NHGRI), Shitaki Toshiyuki and Piero Carninci (RIKEN) CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be

found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

plate: LLAM11762 row: j column: 19

High quality sequence stop: 816.

Location/Qualifiers

1. 910

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone\_lib="NIH\_MGC\_96"

/tissue\_type="hypothalamus"

/lab\_host="DH10B"

/note="Organ: brain; Vector: pBluescript (modified

pBluescript KS+); Site\_1: BamHI; Site\_2: SalI-XhoI (gtcag

); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTNN-3',

size-selected for average insert size 2.3 kb and

normalized to ROT 5. This is a primary library enriched

for full-length clones and constructed using the

cap-trapper method (Carninci, in preparation). Library

constructed by M. Brownstein (NIMH/NHRI, National

Institutes of Health). Note: this is a NIH\_MGC Library."

BASE COUNT 279 a 200 c 195 g 234 t 2 others

ORIGIN

Query Match

Best Local Similarity 74.0%; Score 168.8; DB 10; Length 910;

Matches 228; Conservative 0; Mismatches 77; Indels 3; Gaps 1;

QY 183 agccgcgagagagctgcacactcttcagagaggtccagagagactcaaggagaagat 242

DB 105 AGCCGCGAACAAGACAAAGCTTCACAGAGTCAAGAAAGCAACTCAAGAAATGAT 164

QY 243 agaacacctcaaccttgtagcagagaaatcaaaagagcagagagcttctacagaa 302

DB 165 AGAAACCTTGCTCGGAAGCTGAATGAGAAATCAAGAAATGCAACTTCACAACCA 224

QY 303 gaatcagaacctcaagaagccctgcagaagagcttcaactttcaggtctgttcaca 362

DB 225 GAATCTGAATCTCAAGAAACACTGAAGAGATGCAAAATTTGTCAGCTCTGTCGCA 284

QY 363 agactgctgcagataaagaacgtctacccctt--ccatgggccccttgctgcaga 419

DB 285 AGACTGATATGGCATGAGAAACCTGTTACTATTCTTCGCGCTCATTTAACTGGGA 344

QY 420 aaaaacccgagacacctgcacactcttgaggctgagcttactacaatlaatgtgcaga 479

DB 345 AAAGAGCACAAGAGAGTGTGTTGATGCGCAAGTTCTGAATAATTAAATGACACAGC 404

Y 480 tgatctga 487

DB 405 TGATCTGA 412

RESULT 13

BI289895/c 526 bp mRNA linear EST 19-JUL-2001

LOCUS BI289895 UI-R-DKO-cfp-e-07-0-UI.s1 UI-R-DKO Rattus norvegicus cDNA clone

DEFINITION UI-R-DKO-cfp-e-07-0-UI 3', mRNA sequence.

ACCESSION BI289895

VERSION BI289895.1 GI:14947938

KEYWORDS

EST.

SOURCE

ORGANISM

Rattus

Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

Rattus

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

97044477

COMMENT

Contact: Soares, MB

Program for Rat Gene Discovery and Mapping

University of Iowa

451 Eckstein Medical Research Building Iowa City, IA 52242, USA

Tel: 319 335 8250

Fax: 319 335 9565

Email: msoares@blue.weeg.uiowa.edu

The sequence contained an oligo-dT track that was present in the

oligonucleotide that was used to prime the synthesis of first

strand cDNA and therefore this may represent a bonafide poly A

tail. The sequence tag present in the cDNA between the NotI site

and the oligo-dT track served to identify it as a clone from the

normalized rat placenta pool library cDNA Library Preparation: M.B.

Soares Lab Clone distribution: clones will be available through

Research Genetics (www.resgen.com)

Seq primer: M13 Forward

POLVA-Yes.

FEATURES

source

Location/Qualifiers

1. 526

/organism="Rattus norvegicus"

/strain="Sprague-Dawley"

/db\_xref="taxon:10116"

/clone="UI-R-DKO-cfp-e-07-0-UI"

/clone\_lib="UI-R-DKO"

/dev\_stage="ADULT"

/lab\_host="DH10B (Life Technologies)"

/note="Vector: pTR3D-Pac (Pharmacia) with a modified

polylinker; Site\_1: Not I; Site\_2: Eco RI; The UI-R-DKO

library is a subtracted library derived from a mixture of

five individually tagged normalized rat libraries:

brain-nRBP (20%), heart-nRBP (20%), kidney-nRBP (20%),

aorta-nRBP (20%), and placenta-nRBP (20%). Each original

library was constructed from a mixture of equal amounts of

RNA from seven different developmental time-points:

embryonic day 17, embryonic day 19, embryonic day 21,

adult day 1, adult day 12, adult day 75, and adult day

200. (Exception: the aorta pool does not contain embryonic

day 17 RNA and the placenta pool contains only the three

embryonic stages). Each library was normalized

individually according to the procedure described by

Bonaldo, Lennon & Soares (Genome Research Genome 6:

791-806, 1996). For construction of the DKO subtracted

library, plasmid DNA from each of the five individually

tagged normalized libraries was mixed in the proportions

specified above and electroporated into competent bacteria

for production of single-stranded circular DNA

representing the pool of libraries. Single-stranded

circular DNA representing these five normalized libraries

was then used as a tracer in a subtractive hybridization

with a driver (PCR amplified inserts from a plasmid DNA

template preparation) comprising: a) a set of about 1,000

arrayed clones from each of the five non-normalized

libraries of brain (CROs), heart (CSOs), kidney (CROs),

aorta (CWOs), and placenta (CROs). The resulting pool of

approximately 5,000 clones represented about 33.3% of the

final driver population. A set of about 2,000 arrayed

clones from each of the five normalized libraries of brain

(CROs), heart (CSO), kidney (CRO), aorta (CWO), and

placenta (CRO). The resulting pool of about 10,000 clones

represented about 66.6% of the final driver population.

TAG\_LIB=UI-R-DKO

TAG\_TISSUE=rat placenta pool

TAG\_SEQ=TCACGACAGT"

BASE COUNT 152 a 102 c 113 g 159 t

ORIGIN

QY

542 atcggaagagcctgcacacatgctatggaatgaactcttgaatttcaat 601

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Query Match 20.6%; Score 153.4; DB 10; Length 526;

Best Local Similarity 84.7%; Pred. No. 7.4e-31;

Matches 172; Conservative 0; Mismatches 31; Indels 0; Gaps 0;

QY 542 atcggaagagcctgcacacatgctatggaatgaactcttgaatttcaat 601

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Query Match 18.88; Score 140; DB 10; Length 472

```

/organism="Homo sapiens"
/db_xref="GDB:479199"
/db_xref="taxon:9606"
/clone="IMAGE:127038"
/clone.lib="scores fetal liver spleen INFLS"
/sex="male"
/dev_stage="20 week post conception fetus"
/lab_host="DH10B (ampicillin resistant)"
/note="Organ: Liver and Spleen; Vector: p773D (Pharmacia) with a modified polylinker; Site.1: Pac I; Site.2: Eco RI; 5' strand cDNA was primed with a Pac I - oligo(dCT) primer"

```



GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 19, 2002, 21:57:38 ; Search time 60.72 Seconds

(without alignments)  
451.832 Million cell updates/sec

Title: US-09-898-554-14

Perfect score: 1319

Sequence: 1 MTFDDKMKPANDPEPQKSCG.....ENCILIAFSICQKTNHLQI 247

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : A\_Geneseq\_032802.\*

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22: /SIDSL1/gcgdata/geneseq/geneseq-emb1/AA2001.DAT.*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Length	ID	Description
1	972	73.7	364	22 AAB85873
2	643	48.7	278	22 AAB85871
3	639	48.4	274	22 AAB85872
4	637	48.3	273	17 AAB85869
5	635	48.1	273	20 AAB85869
6	635	48.1	273	20 AAB85869
7	596	45.2	270	17 AAB85869
8	596	45.2	270	20 AAB85869
9	596	45.2	270	20 AAB85869
10	594.5	45.1	273	17 AAB85869
11	582	44.1	20	AAV24153

12	258	19.6	247	20	AAV27448	Human SDCMP4 polyp
13	258	19.6	247	20	AAV27389	Human DC3 protein
14	251	19.0	201	19	AAV52837	Human C-type lectin
15	251	19.0	201	20	AAV27449	Human SDCMP4 short
16	251	19.0	201	20	AAV41764	Human PRO1082 prot
17	251	19.0	201	20	AAV43888	Human DC3 protein
18	251	19.0	201	21	AAV44320	Human PRO1082 (UNO
19	251	19.0	201	22	AAV29077	Human PRO polypept
20	241	18.3	281	22	AAE11943	Human PRO polypept
21	241	18.3	288	22	AAE11926	Human CG27 (or C86
22	241	18.3	307	22	AAE11939	Human CG27 (or C86
23	241	18.3	314	22	AAE11933	Human CG27 (or C86
24	231.5	17.6	180	19	AAV69236	Mouse dectin-1 His
25	231	17.5	176	19	AAV63012	Mouse dectin-1 ext
26	231	17.5	244	19	AAV63009	Mouse dectin-1. M
27	223	16.9	404	21	AAV19714	Dendritic cell spe
28	223	16.9	404	21	AAV28614	Human C-type lecti
29	223	16.9	404	22	AAV79086	Human DC-SIGN, a d
30	221	16.8	247	22	AAE11934	Human CG27 (or C86
31	221	16.8	280	20	AAV05317	Human secreted pro
32	221	16.8	280	21	AAV42619	Human ORFX ORF2383
33	221	16.8	280	21	AAV67228	Membrane-bound pro
34	221	16.8	280	22	AAE11932	Human CG27 (or C86
35	221	16.8	280	22	AAE11938	Human lipid metabo
36	221	16.8	280	22	AAU29324	Human PRO polypept
37	221	16.8	280	22	AAV93544	Human polypeptide,
38	221	16.8	280	22	AAU12400	Human PRO1131 poly
39	221	16.8	280	22	AAV65251	Human PRO1131 (UNO
40	221	16.8	280	22	AAV50959	Human PRO1131 prot
41	221	16.8	284	20	AAV31622	Human oxidised LDL
42	214	16.2	194	19	AAV63016	Mouse dectin-1 iso
43	212	16.1	404	14	AAV32188	Sequence of a non-
44	207	15.7	126	19	AAV63013	Mouse dectin-1 car
45	195.5	14.8	229	22	AAU02496	Murine secreted pr

#### ALIGNMENTS

```

RESULT 1
AAB85873 standard; Protein; 364 AA.
ID AAB85873;
AC AAB85873;
DE 30-NOV-2001 (first entry)
DT Rat LOX-1 polypeptide.
XX
XX
XX LOX-1; LDL; monoclonal antibody; low density lipoprotein; human;
XX atherosclerosis; cardiovascular; kidney disease; inflammatory disorder;
XX leukocyte; rat.
XX
XX Rattus norvegicus.
XX
XX
XX W0200164862-A1.
XX
XX
XX 07-SEP-2001.
XX
XX
XX 02-MAR-2001; 2001WO-JP01636.
XX
XX
XX 02-MAR-2000; 2000JP-0057745.
XX
XX 31-OCT-2000; 2000JP-0333116.
XX
XX (ABGE-) ABGENIX INC.
XX
XX Kobayashi Y, Tsuji H, Kamada M, Sawamura T;
XX WPI: 2001-565503/63.
XX N-PSDB: AAH47114.
XX
XX Human monoclonal antibodies recognizing oxidized low density
XX lipoprotein receptor for treatment of atherosclerosis and
XX
XX

```

PA	(ABGE-)	ABGENIX INC.
XX		
EI	Kobayashi Y,	Tsuji H, Kanada M, Sawamura T;
XX		
DR	WPI; 2001-565503/63.	
DR	N-PSDB; AAH47112.	
XX		
PT	Human monoclonal antibodies recognizing oxidized low density	
PT	lipoprotein receptor for treatment of atherosclerosis and	
PT	cardiovascular and kidney diseases -	
PS	Disclosure; Page 105-108; 131pp; Japanese.	
XX		
CC	The invention provides human monoclonal antibodies and their fragments	
CC	binding to human oxidized low density lipoprotein (LDL) receptor (LOX-1),	
CC	and inhibiting intracellular binding of the receptor to oxidized LDL.	
CC	Drug compositions containing the MAb are useful in the treatment and	
CC	prevention of atherosclerosis, cardiovascular and kidney diseases,	
CC	inflammatory disorders and infiltration of leukocytes. The present	
CC	sequence represents an O. cuniculus LOX-1 polypeptide.	
SO	Sequence    278 AA;	
QY	Query Match	48.7%; Score 643; DB 22; Length 278;
Dd	Best Local Similarity     49.3%; Pred. No. 5,6e-46;	
Matches	135; Conservative    39; Mismatches    70; Indels    30; Gaps        6	
QY	1 MTFFD-KKKRPADDEDDKSCGCKPKKEESORELK-----GKITITR----	40
Dd	5 mavedllkxpmkdqpdqksngkkpk--glrlfsspwcpaaavalyclgslmtlmigm	62
QY	41 --KUDESKQEDELQMIQNLE---AIQRANSSSEDSRELGKIDTLTFLKNESK	93
Dd	63 qllqysdlkkqqanliltgenilleqvylaqqaesaasgesqlkemietlakrideak	122
QY	94 EOEELQKNQNLQEALQRANSFGPCPODWLMHKENCYLF-HGFWEKNRQTOSLGGO	152
Dd	123 kqmelnhbylnlqealktmdnltspopedwlwhgnkyilfssgsfnwessgeklsladaq	182
QY	153 LIOINGADDLPFIQAISHTTSPFWIGLRHRKKGOPMLMENGPPLNFQPFKTRGVSLQLY	212
Dd	183 llkinstedlgigtatshsfymglstrkrpdyawlwedgsplmhlfrfgavsqrty	242
QY	213 SSSNCAYLQDGAVFAENCLIAFASICQKKTNNHQ	246
Dd	243 psytcaiyikgnvfaencillvaaysicqkkanllr	276
RESULT	3	
AAB85872	AAB85872 standard; Protein; 274 AA.	
AC	AAB85872;	
XX		
DT	30-NOV-2001 (first entry)	
XX		
DE	S. scrofa LOX-1 polypeptide.	
XX		
KM	LOX-1; LDL; monoclonal antibody; low density lipoprotein; human;	
KW	atherosclerosis; cardiovascular; kidney disease; inflammatory disorder;	
Lekocyte.		
XX	Sus scrofa.	
OS		
PN	MO200164862-A1.	
XX		
PD	07-SEP-2001.	
XX		
FE	02-MAR-2000; 2000JP-0057745.	
RR	31-OCT-2000; 2000JP-0333116.	



XX (ABGE-) ABGENIX INC.  
 PA Kobayashi Y, Tsuji H, Kamada M, Sawamura T;  
 XX WPI; 2001-565503/63.  
 DR N-PSDB; AAA47113.  
 XX  
 PT Human monoclonal antibodies recognizing oxidized low density  
 PT lipoprotein receptor for treatment of atherosclerosis and  
 PT cardiovascular and kidney diseases  
 XX  
 PS Disclosure; Page 111-115; 131pp; Japanese.  
 XX  
 CC The invention provides human monoclonal antibodies and their fragments  
 CC binding to human oxidized low density lipoprotein (LDL) receptor (LOX-1),  
 CC and inhibiting intracellular binding of the receptor to oxidized LDL.  
 CC Drug compositions containing the MAb are useful in the treatment of  
 CC prevention of atherosclerosis, cardiovascular and kidney diseases,  
 CC inflammatory disorders and infiltration of leukocytes. The present  
 CC sequence represents a S. scrofa LOX-1 polypeptide.  
 XX  
 SQ Sequence 274 AA;

Query Match 48.4%; Score 639; DB 22; Length 274;  
 Best Local Similarity 47.3%; Pred. No. 1.2e-45;  
 Matches 131; Conservative 37; Mismatches 73; Indels 36; Gaps 5;

QY 1 MTFDD-KMKRANDEPDOKSCGKPKRESORELK-----GKIDT-- 32  
 Db 1 mtfddkismkmdqpdksng--dkaegprslslrwrpaalllgllclglvltvllll 58  
 QY 33 --GKIDITRKLDEKSKROEELQMIQ--EALORANSSSESOBELKGIIDTLTKINE 90  
 Db 59 qlsvsdllyqkvklthgedil--egqalagrqaeksqsgreltemletlakhide 115  
 QY 91 KSKOEELLOKNQNLQALORANFSGPCPODWLHKENCYLF-HGPGWEKNRQTCOSL 149  
 Db 116 ksklmeqlqgnlnlqelalekaanfsgpcpqlwhencykfsqpsfweksreclsl 175  
 QY 150 GGQLQINGADDLFTLLQALISHTTSPFWIGLHRRKPGOPWLMENGTPLNFGFFKTRGVSL 209  
 Db 176 daqlilkinstadlfiqtlahsfpfwmjgslrkpnswlwedgplmpflfrvgaas 235  
 QY 210 QLYSSNCAYLQDGAFAENCILIAFSICOKKTNHLQ 246  
 Db 236 qmypsqtcaylhrgivtaencilnaafsicqkranllr 272

RESULT 4  
 ID AAR9588 standard; Protein; 273 AA.  
 AC AAR9588;  
 DT 29-OCT-1996 (first entry)  
 DE Low density lipoprotein receptor.  
 KW LDL; low density lipoprotein; receptor; bovine; assay; detection;  
 KW recombinant production; haemangioendothelial cell.  
 OS Homo sapiens.  
 PN WO9617058-A1.  
 PD 06-JUN-1996.  
 PF 30-NOV-1995; 95WO-JP02444.  
 PR 31-JUL-1995; 95JP-0214206.  
 PR 30-NOV-1994; 94JP-0321705.

XX (NIMC) NIPPON CHEMIPHAR CO.  
 PA Masaki T, Sawamura T;  
 XX WPI; 1996-277778/28.  
 DR N-PSDB; AAT32578.  
 XX  
 PT DNA encoding denatured low-density lipoprotein receptor of mammalian  
 PT haemangioendothelial cells - useful for generating antibodies for  
 PT use in detection of LDL in biological samples  
 XX  
 PS Claim 1; Page 31-34; 44pp; Japanese.  
 XX  
 CC The present sequence is that of a human denatured low density  
 CC lipoprotein (LDL) receptor encoded by DNA isolated from  
 CC haemangioendothelial cells. The DNA is useful for the production of  
 CC the receptor protein in transformed hosts. Antibodies to the protein  
 CC are useful in detection and assays of LDL in biological samples.  
 XX  
 SQ Sequence 273 AA;

Query Match 48.3%; Score 637; DB 17; Length 273;  
 Best Local Similarity 48.9%; Pred. No. 1.8e-45;  
 Matches 134; Conservative 35; Mismatches 69; Indels 36; Gaps 6;

QY 1 MTFDD-KMKRANDEPDOKSCGKPKRESORELK-----GKIDT-- 38  
 Db 1 mtfddkikqlykvkdqpdksngkkak---glqfyspwwclaaatlglvclglvltmv 55  
 QY 39 -----TRKLDEKSKROEELQMIQ--EALORANSSSESOBELKGIIDTLTKINE 90  
 Db 56 lymqtsqvsdlitqganltqkkllegqisargaaesgesenletlarkline 115  
 QY 91 KSKOEELLOKNQNLQALORANFSGPCPODWLHKENCYLF-HGPGWEKNRQTCOSL 149  
 Db 116 kskemelhqgnlnlqelkryancapcpqqlwhgencylfssgfnweksgeklsl 175  
 QY 150 GGQLQINGADDLFTLLQALISHTTSPFWIGLHRRKPGOPWLMENGTPLNFGFFKTRGVSL 209  
 Db 176 daklilkinstadlfiqalisyssfpwmjgslrpnswlwedgplmpflfrvgaas 235  
 QY 210 QLYSSNCAYLQDGAFAENCILIAFSICOKKTN 243  
 Db 236 qlypsqtcaylqrgavyaencilnaafsicqkkan 269

RESULT 5  
 ID AAB85869 standard; Protein; 273 AA.  
 AC AAB85869;  
 DT 30-NOV-2001 (first entry)  
 DE Human LOX-1 polypeptide.  
 KW LOX-1; LDL; monoclonal antibody; low density lipoprotein; human;  
 KW atherosclerosis; cardiovascular; kidney disease; inflammatory disorder;  
 KW leukocyte.  
 OS Homo sapiens.  
 PN WO200164862-A1.  
 PD 07-SEP-2001.  
 PF 02-MAR-2001; 2001WO-JP01636.  
 PR 02-MAR-2000; 2000JP-0057745.  
 PR 31-OCT-2000; 2000JP-0333116.

PA (ABGE-) ABGENIX INC.  
 XX Kobayashi Y, Tsuji H, Kamada M, Sawamura T;  
 XX  
 XX WPI: 2001-565503/63.  
 DR N-PSDB; AAA47105.  
 XX  
 XX Human monoclonal antibodies recognizing oxidized low density  
 PT lipoprotein receptor for treatment of atherosclerosis and  
 PT cardiovascular and kidney diseases  
 XX  
 PS Disclosure: Page 87-92; 131pp; Japanese.  
 XX  
 CC The invention provides human monoclonal antibodies and their fragments  
 CC binding to human oxidized low density lipoprotein (LDL) receptor (LDX-1),  
 CC and inhibiting intracellular binding of the receptor to oxidized LDL.  
 CC Drug compositions containing the Mab are useful in the treatment and  
 CC prevention of atherosclerosis, cardiovascular and kidney diseases,  
 CC inflammatory disorders and infiltration of leukocytes. The present  
 CC sequence represents a human LDX-1 polypeptide.  
 XX  
 CC Sequence 273 AA:

Query Match 48.3%; Score 637; DB 22; Length 273;  
 Best Local Similarity 48.9%; Pred. No. 1.8e-45;  
 Matches 134; Conservative 35; Mismatches 69; Indels 36; Gaps 6;

QY 1 MTFDD-KMKPANDPPQSGKKPKESORELK-----GKIDT-- 38  
 DB 1 mtfddkikgtvkdpqeksnqkkak-----gldflyspwwcilaatlgyviclgivltlmv 55  
 QY 39 -----TRKLDKSKSEOEELLQMIQNLQ---EALQRAANSSEESORELKIDITLTKLNE 90  
 DB 56 lmqqlsqvsdjlitqeganltqgkkllegqtsarqaeasqesenelekmetlarkline 115  
 QY 91 KSKOEELLQKNONLOEALQRAANFSGPCPDMLMKENCYLF-HGPFGEKRRQTCOSL 149  
 DB 116 kskqemelhqgnlnlqetlkrvancsapcpqdwlmhngencyltsqsfmweksqekclsl 175  
 QY 150 GGOLQINGADDLFTILQAIISHTTSPFWIGLHRRKKGQPLWMENGTPPLNFOFKTRGVSL 209  
 DB 176 dakllkinstadldfqqatsysfpmglstrnpsypwlvwedgspjlmphlfrvrgavs 235  
 QY 210 QLYSSNCAYLQDGAFAENCILIAFSICQKTN 243  
 DB 236 qlypsgtcaylqrgavyaencillaatsicqkkan 269

RESULT 6  
 ID AAY24151  
 AC AAY24151; standard; Protein; 273 AA.

XX  
 XX 10-SEP-1999 (first entry)  
 XX  
 XX Human LDL receptor.  
 XX  
 XX Human; LDL; denatured; oxidized; arteriosclerosis; hyperlipidaemia;  
 KW low density lipoprotein; receptor; detection; immunoglobulin;  
 KM fusion protein.  
 XX  
 XX Homo sapiens.  
 OS  
 XX  
 XX WO9332520-A1.  
 PN  
 XX  
 XX 01-JUL-1999.  
 PD  
 XX  
 XX 18-DEC-1998; 98WO-JP05744.  
 PF  
 XX  
 XX 16-DEC-1998; 98JP-0358170.  
 PR  
 XX 19-DEC-1997; 97JP-0364981.

PR 09-DEC-1998; 98JP-0349648.  
 XX  
 XX (NISB) JAPAN TOBACCO INC.  
 XX  
 XX  
 XX Kakutani M, Masaki T, Sawamura T;  
 PI  
 XX  
 XX WPI: 1999-418906/35.  
 DR N-PSDB; AAX88527.  
 XX  
 XX Fusion peptide for assay of oxidized LDL and for therapeutic use  
 PT  
 PS Claim 9; Page 71-73; 105pp; Japanese.  
 XX

CC The present invention describes a fusion peptide which consists of the  
 CC extracellular domain of a mammalian oxidized LDL (low density  
 CC lipoprotein) receptor, fused to a partial heavy chain of a mammalian  
 CC immunoglobulin containing all or part of the constant region. Oxidized  
 CC LDL is a denatured form of LDL occurring in patients having  
 CC arteriosclerosis or hyperlipidaemia, and the fusion peptide can be  
 CC used for the assay of oxidized LDL in biological samples from such  
 CC patients, for the diagnosis of the disorders. It can also be used  
 CC therapeutically for the prevention and treatment of arteriosclerosis and  
 CC hyperlipidaemia. The present sequence represents the human LDL receptor.  
 CC  
 CC Sequence 273 AA:

Query Match 48.1%; Score 635; DB 20; Length 273;  
 Best Local Similarity 48.5%; Pred. No. 2.6e-45;  
 Matches 133; Conservative 36; Mismatches 69; Indels 36; Gaps 6;

QY 1 MTFDD-KMKPANDPPQSGKKPKESORELK-----GKIDT-- 37  
 DB 1 mtfddkikgtvkdpqeksnqkkak-----gldflyspwwcilaatlgyviclgivltlmv 55  
 QY 38 -----TRKLDKSKSEOEELLQMIQNLQ---EALQRAANSSEESORELKIDITLTKLNE 90  
 DB 56 lmqqlsqvsdjlitqeganltqgkkllegqtsarqaeasqesenelekmetlarkline 115  
 QY 91 KSKOEELLQKNONLOEALQRAANFSGPCPDMLMKENCYLF-HGPFGEKRRQTCOSL 149  
 DB 116 kskqemelhqgnlnlqetlkrvancsapcpqdwlmhngencyltsqsfmweksqekclsl 175  
 QY 150 GGOLQINGADDLFTILQAIISHTTSPFWIGLHRRKKGQPLWMENGTPPLNFOFKTRGVSL 209  
 DB 176 dakllkinstadldfqqatsysfpmglstrnpsypwlvwedgspjlmphlfrvrgavs 235  
 QY 210 QLYSSNCAYLQDGAFAENCILIAFSICQKTN 243  
 DB 236 qlypsgtcaylqrgavyaencillaatsicqkkan 269

RESULT 7  
 ID AAR9586  
 AC AAR9586; standard; Protein; 270 AA.

XX  
 XX 29-OCT-1996 (first entry)  
 XX  
 XX Low density lipoprotein receptor.  
 XX  
 XX LDL; low density lipoprotein; receptor; bovine; assay; detection;  
 KW recombinant production; haemangioendothelial cell.  
 KM  
 XX  
 XX Bos taurus.  
 OS  
 XX  
 XX WO9617058-A1.  
 PN  
 XX  
 XX 06-JUN-1996.  
 PD  
 XX  
 XX 30-NOV-1995; 95WO-JP02444.  
 PF  
 XX

PR 31-JUL-1995; 95JP-0214206.  
PR 30-NOV-1994; 94JP-0321705.  
XX  
PA (NICH ) NIPPON CHEMIPHAR CO.  
XX  
PI Masaki T, Sawamura T;  
XX  
XX WPI: 1996-277778/28.  
DR N-PSDB: AAT32576.  
XX  
PT DNA encoding denatured low-density lipoprotein receptor of mammalian  
PT haemangioendothelial cells - useful for generating antibodies for  
PT use in detection of LDL in biological samples  
XX  
XX  
PS Claim 1; Page 22-26; 44pp; Japanese.  
XX  
XX The present sequence is that of a bovine denatured low density  
CC lipoprotein (LDL) receptor encoded by DNA isolated from  
CC haemangioendothelial cells. The DNA is useful for the production of  
CC the receptor protein in transformed hosts. Antibodies to the protein  
CC are useful in detection and assays of LDL in biological samples.  
XX  
SQ Sequence 270 AA;

Query Match 45.2%; Score 596; DB 17; Length 270;  
Best Local Similarity 44.6%; Pred. No. 4.7e-42;  
Matches 125; Conservative 39; Mismatches 70; Indels 46; Gaps 6;

OY 1 MTFDDKMKRANDEPDOKSGKKPK-----EESQR 29  
Db 1 mtfvddp-kymkdqldqkpnktakgfvswrwyapaavlgycljllvtvlllllqlsq- 58  
OY 30 ELKGRIDITRKLDKSKKEQELL--QMIONLOEALQRAANSSESSORELKGIDITRLK 87  
Db 59 -----vsdlkkqgnlthgedilegqll-----agrrseksaagesqkelkemieltahk 108  
OY 88 INEKSKEQELLQKNONLOEALQRAANSFGPCPDMLMKENCYLF-HGPFGEKRNROTG 146  
Db 109 ldekskkmelhrgnlhqlgevlkeaanysgpcpqdwlwheencyfssgfnweksqenc 168  
OY 147 OSLSGQLQINGADDLFTFLQAIISHTTSPFWIGLHRRKRGQWLMENGTPLNFOEFKTRG 206  
Db 169 lsdahlliklnstdeletiqmiahnsfpfwmglmsmrkpnyswlwedgtpltpnlfrlqg 228  
OY 207 VSLQLYSSNCAYLQDGAFFAENCILIAFSICOKKTNHLQ 246  
b 229 avsrmypsgtcaylqrgtvaencillatatsicqkkanllr 268

RESULT 8  
AAY24152  
ID AAY24152 standard; Protein: 270 AA.  
XX  
AC AAY24152;  
XX  
DT 10-SEP-1999 (first entry)  
XX  
DE Bovine LDL receptor.  
XX  
XX LDL; denatured; oxidised; arteriosclerosis; hyperlipidaemia;  
KM low density lipoprotein; receptor; detection; immunoglobulin;  
fusion protein.  
XX  
OS Bos sp.  
XX  
PN WO9932520-A1.  
XX  
PD 01-JUL-1999.  
XX  
PF 18-DEC-1998; 98MO-JP05744.  
XX  
PR 16-DEC-1998; 98JP-0358170.

PR 19-DEC-1997; 97JP-0364981.  
PR 09-DEC-1998; 98JP-0349648.  
XX  
PA (NITSB ) JAPAN TOBACCO INC.  
XX  
XX Kakutani M, Masaki T, Sawamura T;  
XX  
XX WPI: 1999-418906/35.  
DR N-PSDB: AAB85870.  
XX  
XX Fusion peptide for assay of oxidized LDL and for therapeutic use  
PT  
PS Claim 11; Page 73-75; 105pp; Japanese.  
XX  
XX

The present invention describes a fusion peptide which consists of the extracellular domain of a mammalian oxidized LDL (low density lipoprotein) receptor, fused to a partial heavy chain of a mammalian immunoglobulin containing all or part of the constant region. Oxidized LDL is a denatured form of LDL occurring in patients having arteriosclerosis or hyperlipidaemia, and the fusion peptide can be used for the assay of oxidized LDL in biological samples from such patients, for the diagnosis of the disorders. It can also be used therapeutically for the prevention and treatment of arteriosclerosis and hyperlipidaemia. The present sequence represents the bovine LDL receptor.

Query Match 45.2%; Score 596; DB 20; Length 270;  
Best Local Similarity 44.6%; Pred. No. 4.7e-42;  
Matches 125; Conservative 39; Mismatches 70; Indels 46; Gaps 6;

OY 1 MTFDDKMKRANDEPDOKSGKKPK-----EESQR 29  
Db 1 mtfvddp-kymkdqldqkpnktakgfvswrwyapaavlgycljllvtvlllllqlsq- 58  
OY 30 ELKGRIDITRKLDKSKKEQELL--QMIONLOEALQRAANSSESSORELKGIDITRLK 87  
Db 59 -----vsdlkkqgnlthgedilegqll-----agrrseksaagesqkelkemieltahk 108  
OY 88 INEKSKEQELLQKNONLOEALQRAANSFGPCPDMLMKENCYLF-HGPFGEKRNROTG 146  
Db 109 ldekskkmelhrgnlhqlgevlkeaanysgpcpqdwlwheencyfssgfnweksqenc 168  
OY 147 OSLSGQLQINGADDLFTFLQAIISHTTSPFWIGLHRRKRGQWLMENGTPLNFOEFKTRG 206  
Db 169 lsdahlliklnstdeletiqmiahnsfpfwmglmsmrkpnyswlwedgtpltpnlfrlqg 228  
OY 207 VSLQLYSSNCAYLQDGAFFAENCILIAFSICOKKTNHLQ 246  
Db 229 avsrmypsgtcaylqrgtvaencillatatsicqkkanllr 268

RESULT 9  
AAB85870  
ID AAB85870 standard; Protein: 270 AA.  
XX  
AC AAB85870;  
XX  
DT 30-NOV-2001 (first entry)  
XX  
DE Bovine LOX-1 polypeptide.  
XX  
XX LOX-1; LDL; monoclonal antibody; low density lipoprotein; human;  
KM arteriosclerosis; cardiovascular; kidney disease; inflammatory disorder;  
leukocyte; bovine.  
XX  
OS Bos taurus.  
XX  
PN WO200164862-A1.  
XX  
PD 07-SEP-2001.  
XX



PF 18-DEC-1998; 98WO-JP05744.  
 XX  
 PR 16-DEC-1998; 98JP-0358170.  
 PR 19-DEC-1997; 97JP-0364981.  
 PR 09-DEC-1998; 98JP-0349648.  
 XX  
 PA (NIBS ) JAPAN TOBACCO INC.  
 XX  
 PI Kakutani M, Masaki T, Sawamura T;  
 XX  
 DR WPI: 1999-418906/35.  
 DR N-PSDB; AAX85529.  
 XX  
 PT Fusion peptide for assay of oxidized LDL and for therapeutic use  
 XX  
 PS Claim 12; Page 75-79; 105pp; Japanese.  
 XX  
 CC The present invention describes a fusion peptide which consists of the  
 CC extracellular domain of a mammalian oxidized LDL (low density  
 CC lipoprotein) receptor, fused to a partial heavy chain of a mammalian  
 CC immunoglobulin containing all or part of the constant region. Oxidized  
 CC LDL is a denatured form of LDL occurring in patients having  
 CC arteriosclerosis or hyperlipidaemia, and the fusion peptide can be  
 CC used for the assay of oxidized LDL in biological samples from such  
 CC patients, for the diagnosis of the disorders. It can also be used  
 CC therapeutically for the prevention and treatment of arteriosclerosis and  
 CC hyperlipidaemia. The present sequence represents a chimeric protein  
 CC comprising the bovine LOX-1 extracellular region and the human  
 CC immunoglobulin IgG1 Fc region.  
 CC  
 XX  
 SO Sequence 445 AA;

Query Match 44.1%; Score 582; DB 20; Length 445;  
 Best Local Similarity 52.4%; Pred. No. 1.4e-40;  
 Matches 111; Conservative 36; Mismatches 57; Indels 8; Gaps 3;  
 QY 38 ITRKIDSKDELL--OMIONLOALORANSESEOREKGRIDTLTKNRSKRO 95  
 Db 2 lkkqanltqgedllegql-----agrrseksaqesqekeltahldskskl 56  
 QY 96 EELLOKNOLOALORANFSGPCPODWLHKENCYL- HGFPGWEKNRQTCOSLGGOL 154  
 Db 57 melhgnlnlgevlkeaanysqpcqdwlvheencyqfssgfneksqenclsdanll 116  
 QY 155 OINGADDLFTILOATSHHTSPWIGLHRKKGPOPLWENGCTPLNQFETRGVSIOLYSS 214  
 Db 117 kinstdelefqumlahssfrfmglsmc kpnyswlwedgtrplrlrlgavarsmyps 176  
 QY 215 SNCAYLODGAFAENCILIAFSICQKKTNNLQ 246  
 Db 177 gtcaylgrgtvfaenciltatfscqkanllr 208

RESULT 12  
 AAY27448  
 ID AAY27448 standard; Protein; 247 AA.  
 XX  
 AC AAY27448;  
 XX  
 DT 26-NOV-1999 (first entry)  
 XX  
 DE Human SDCMP4 polypeptide.  
 XX  
 KW Binding compound; antibody binding site; primate; rodent; SDCMP3; SDCMP4;  
 KW Schering dendritic cell membrane protein; dendritic cell physiology;  
 KW genetic fingerprinting; cancer immunotherapy; abnormal proliferation;  
 KW cancer; forensic; human; lectin 47.  
 OS Homo sapiens.  
 XX  
 PF MO9947673-A2.  
 XX

PD 23-SEP-1999.  
 XX  
 PR 16-MAR-1999; 99WO-US03740.  
 XX  
 PR 17-MAR-1998; 98US-0040111.  
 XX  
 PA (SCHE ) SCHERING CORP.  
 XX  
 PI Chalus L, Quan AB, Bates EEM, Gorman DM, Saeland S, Lebecque SJE;  
 PI Philippines JH;  
 XX  
 DR WPI: 1999-562114/47.  
 DR N-PSDB; AAZ07533.  
 XX  
 PT Binding compound specific for primate or rodent Schering dendritic cell  
 XX membrane proteins  
 XX  
 PS Claim 2; Page 84-85; 89pp; English.  
 XX  
 CC The invention relates to a binding compound comprising an antibody  
 CC binding site which specifically binds to: (a) a primate or rodent  
 CC Schering dendritic cell membrane protein 3 (SDCMP3) protein; or (b) a  
 CC primate SDCMP4 protein. The binding compound can be used to modulate  
 CC dendritic cell physiology or function. The sequences may also be used as  
 CC probes in forensic techniques, such as genetic fingerprinting. They can  
 CC also be used to distinguish tissue and cell types in situ or in vitro.  
 CC The sequences may also be useful in cancer immunotherapy and in the  
 CC treatment of conditions associated with abnormal physiology or  
 CC development, including abnormal proliferation, e.g. cancerous conditions,  
 CC or degenerative conditions. The present sequence represents the human  
 CC SDCMP4 polypeptide (lectin 47).  
 CC  
 XX  
 SO Sequence 247 AA;

Query Match 19.6%; Score 258; DB 20; Length 247;  
 Best Local Similarity 31.2%; Pred. No. 9.5e-14;  
 Matches 50; Conservative 41; Mismatches 65; Indels 4; Gaps 3;  
 QY 86 LKLNESKRO--EELLOKNOLOALORANFSGPCPODWLHKENCYLHGFPGWEKN 142  
 Db 85 lsrnkenhsqptqslsdevsrptkavktgvlsspprmvlyexscylfmslnswdgs 144  
 QY 143 ROTCOSLGGOLQINGADDLFTIL-OAISHHTSPWIGLHRKKGPOPLWENGCTPLNQF 201  
 Db 145 kqcgqqlgnllkldesnldfivqvsqpnstfvlgsrptqewplwedgstssnl 204  
 QY 202 FETRGVSIOLYSSSNCAYLODGAFAENCILIAFSICQK 241  
 Db 205 fglttatqenpsncwlvhsvlydqslsvpsysicekk 244

RESULT 13  
 AAW73889  
 ID AAW73889 standard; Protein; 247 AA.  
 XX  
 AC AAW73889;  
 XX  
 DT 31-MAR-1999 (first entry)  
 XX  
 DE Human DC3' protein sequence.  
 XX  
 KW Dendritic cell-derived membrane protein; human; DC3'.  
 OS Homo sapiens.  
 XX  
 PN JP11001497-A.  
 XX  
 PD 06-JAN-1999.  
 XX  
 PF 13-JUN-1997; 97JP-0156376.  
 XX  
 PR 13-JUN-1997; 97JP-0156376.  
 XX

XX	(TAKE ) TAKEDA CHEM IND LTD.
PA	
XX	WI; 1999-125479/11.
DR	N-PSDB; NAX01260.
XX	
XX	New membrane protein and its DNA - useful as reagents for screening
PT	ligand, agonist or antagonist
XX	
PS	Claim 1; Page 37-38; 44pp; Japanese.
CC	This sequence is the human dendritic cell-derived membrane protein
CC	DCJ' of the invention. The protein, its fragments and salts are useful a
CC	reagents for screening a ligand, an agonist or an antagonist DC3.
XX	
SQ	Sequence    247 AA;
OY	Query Match                      19.6%; Score 258; DB 20; Length 247; Best Local Similarity    31.2%; Pred. No. 9,5e-14; Matches    50; Conservative    41; Mismatches    65; Indels     4; Gaps
Db	86 LKLEKSEKQ--EELLOKRNQLDQALORANFSGPCPDMLMHKENCYLFHGPF-GWEKN 142  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  ::: 85 lsrkhemisptqlssledsvprtkavktlgtvlsppcpnwliyekscylfsmslnswdgs 144
OY	143 ROTCOSSLGQLLIINGADDLFEFL-QAISHTSPFWIGLHRKKRGPQWLMENGSTPLNPOF 201 :::      :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  ::: Db    145 krqcgwqysnlkkidsrnejgfykyvsqpdsnfwiqlsrpqetvpwlwedgstlssml 204 202 FKTRGVSLQLYSSNCAYLDGAVFAENCILIAFSICOKR 241  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  :::  ::: Db    205 fglrtatqenpspcwihvsiydgllcspsysiceck 244
RESULT 14	
AAM52837	ID AAM52837 standard; Protein; 201 AA.
XX	AAM52837;
AC	
XX	24-JUN-1998 (first entry)
DT	
XX	Human C-type lectin MCTL.
DE	
XX	C-type lectin; MCTL; type II membrane protein; antibody;
KW	diagnosis; Antisense; allograft; macrophage.
KW	
XX	Homo sapiens.
OS	
XX	WO9802456-A2.
XX	
PD	22-JAN-1998.
XX	
FF	15-JUL-1997; 97WO-US12342.
XX	
PR	30-JUL-1996; 96US-0688342.
PR	15-JUL-1996; 96US-0683657.
XX	
PA	(INCY-) INCYTE PHARM INC.
XX	
P1	Au-young J, Cocks BG, Goli SK, Hillman JL;
XX	
DR	WI; 1998-110526/10.
DR	N-PSDB; AAV21156.
XX	
PT	Human C-type lectin - useful in, e.g. treating graft rejection,
PT	auto-immune disease and cancer
XX	
PS	Claim 1; Fig 1; 53pp; English.
CC	The Human C-type lectin MCTL protein shows homology to the C-type lectin
CC	superfamily of type II Membrane proteins. Purified MCTL and it's

CC	agonists can be used in the treatment of diseases associated with the
CC	expression of MCTL. MCTL and anti-MCTL antibodies can be used for
CC	diagnosis and monitoring purposes during treatment. Antisense
CC	nucleotides may be used to diminish or prevent allograft rejection and
CC	MCTL inhibitors are useful in the prevention of macrophage colonisation
CC	by pathogenic bacteria.
XX	
SO	Sequence      201 AA:
OY	Query Match                  19.0%; Score 251; DB 19; Length 201;
	Best Local Similarity    35.2%; Pred. No. 2.8e-13;
	Matches    45; Conservative    32; Mismatches    49; Indels     2; Gaps       2
OY	116 SGPQCDWMHMKENCYLFFGPF-GWKKNQTOCSLGGLQINGADDTFIL-QAISHRT 173         : : : :         : : : :         : : : :         : : : :
Db	71 sspcpnnwvlllyekscyllfmslnswgskrrgcqlsnllkldssnelyglfvkvssqpd 130         : : : :         : : : :         : : : :         : : : :
OY	174 SPFWGIHRRKKGOPWLMEWGTPLNFOFKTRGVSLQLTSSNCAYLAGAVFAENCIL 233 :         : : : :         : : : :         : : : :         : : : :
Db	131 nsfwlglsrpgclevpwlwedgstfsnlqgtttatqenpsncvwihnsviydglicsvp 190 : :       : : : :         : : : :         : : : :         : : : :
OY	234 AFSICQKK 241 : :       : : : :         : : : :         : : : :         : : : :
Db	191 sysicekk 198 : :       : : : :         : : : :         : : : :         : : : :
RESULT 15	
AAY27449	
ID	AAY27449 standard; Protein; 201 AA.
XX	
AC	AAY27449;
XX	
DT	26-NOV-1999 (first entry)
XX	
DE	Human SDCMP4 short form polypeptide.
XX	
KW	Binding compound; antibody binding site; primate; rodent; SDCMP3; SDCMP4;
KM	Scherling dendritic cell membrane protein; dendritic cell physiology;
KW	genetic fingerprinting; cancer immunotherapy; abnormal proliferation;
XX	cancer; forensic; human.
XX	
OS	Homo sapiens.
XX	
PN	WO9947673-A2.
XX	
PD	23-SEP-1999.
XX	
PE	16-MAR-1999; 99WO-US03740.
XX	
PR	17-MAR-1998; 98US-0040111.
XX	
PA	(SCHE ) SCHERING CORP.
XX	
PI	Chalus L, Quan AB, Bates EEM, Gorman DM, Saeland S, lebecque SEJ;
PI	Phillips JH;
XX	
DR	WP1; 1999-562114/47.
XX	
N-PSDB;	AAZ07534.
XX	
PT	Binding compound specific for primate or rodent schering dendritic cell
XX	membrane proteins -
Pt	
XX	
PS	Claim 2; Page 87-88; 89pp; English.
XX	
CC	The invention relates to a binding compound comprising an antibody
CC	binding site which specifically binds to: (a) a primate or rodent
CC	Scherling dendritic cell membrane protein 3 (SDCMP3) protein; or (b) a
CC	primate SDCMP4 protein. The binding compound can be used to modulate
CC	dendritic cell physiology or function. The sequences may also be used as
CC	probes in forensic techniques, such as genetic fingerprinting. They can
CC	also be used to distinguish tissue and cell types in situ or in vitro.
CC	The sequences may also be useful in cancer immunotherapy and in the

AA	Sequence	201	AA;
SQ			

Query Match	Score	DB	Length
19.08;	251;	20;	201;
35.08;	251;	20;	201;
35.08;	251;	20;	201;

Best Local Similarity 35.28; Pred. No. 2.8e-13;  
Matches 45; Conservative 32; Mismatches 49; Indels 2; Gaps 2

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QY      116  SGPRPQDWMHKENCYLFGHPP-GWEKRRQTCOSLGGOLQINAGDDTLFLL-QAISHTT 173
      | ||| :: :: |||| | :: | | ||| :: :: | | |
Db      71  sspprnwilyekscylfsmsslnswdskrgcwgqlgsnllkldssnelglfivkvssqpd 130

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174 SPFWIGLHRRKKPGQPLWENGTPLNFOEFKTRGVSLQLYSSNGAYLQDGAVFAENCILI 233

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131 nsfwiglsrptqtevpwlmwedgstffsnlfgirttatqenpsncwlvhsvlydqjcsvp 190

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QY 234 AFSICQK 241

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Db      191 sysicekk 198
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Search completed: August 19, 2002, 22:57:18  
Job time: 3580 sec

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GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 19, 2002, 22:01:29 ; Search time 25.02 Seconds  
(without alignments)  
-241.132 Million cell updates/sec

Title: US-09-898-554-14

Perfect score: 1319

Sequence: 1 MTFDDKMKAPNDPPDKSCG.....ENCILIAFSICQKTNHLQI 247

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

Issued\_Patents\_AA: \*  
1: /cgn2\_6/ptodata/1/1aa/5A\_COMB.pep: \*  
2: /cgn2\_6/ptodata/1/1aa/5B\_COMB.pep: \*  
3: /cgn2\_6/ptodata/1/1aa/6A\_COMB.pep: \*  
4: /cgn2\_6/ptodata/1/1aa/6B\_COMB.pep: \*  
5: /cgn2\_6/ptodata/1/1aa/PCTUS\_COMB.pep: \*  
6: /cgn2\_6/ptodata/1/1aa/Backfile1.pep: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	637	48.3	273	2	US-09-055-095-3
2	637	48.3	273	2	US-08-809-494A-6
3	637	48.3	273	4	US-09-352-302-6
4	596	45.2	270	2	US-09-055-095-4
5	596	45.2	270	2	US-08-809-494A-2
6	596	45.2	270	4	US-09-352-302-2
7	594.5	45.1	273	2	US-08-809-494A-4
8	594.5	45.1	273	4	US-09-352-302-4
9	251	19.0	201	2	US-08-688-342-1
10	251	19.0	201	2	US-09-113-788-1
11	231.5	17.6	180	3	US-08-772-440-31
12	231	17.5	176	3	US-08-772-440-8
13	231	17.5	244	3	US-08-772-440-2
14	221	16.8	284	2	US-09-055-095-1
15	214	16.2	199	3	US-08-772-440-13
16	207	15.7	126	3	US-08-772-440-10
17	189.5	14.4	122	3	US-08-722-126A-9
18	189.5	14.4	122	5	PCT-US95-04258-9
19	186	14.1	272	3	US-08-690-095-1
20	186	14.1	272	3	US-09-113-789-1
21	186	14.1	287	1	US-08-365-103B-4
22	186	14.1	300	1	US-08-365-103B-6
23	186	14.1	327	1	US-08-365-103B-2
24	179	13.6	229	4	US-09-247-155-97
25	166	12.6	179	1	US-08-690-095-9
26	166	12.6	179	1	US-08-650-578-2
27	166	12.6	179	2	US-08-688-342-3

28	166	12.6	179	2	US-09-113-788-3	Sequence 3, Appl
29	166	12.6	179	3	US-09-113-789-9	Sequence 9, Appl
30	165.5	12.5	287	4	US-09-111-470-6	Sequence 6, Appl
31	165.5	12.5	320	1	US-08-365-103B-10	Sequence 10, Appl
32	165.5	12.5	321	1	US-08-365-103B-8	Sequence 8, Appl
33	162.5	12.3	231	1	US-08-690-095-6	Sequence 6, Appl
34	162.5	12.3	231	3	US-09-113-789-6	Sequence 6, Appl
35	162.5	12.3	231	4	US-08-543-246B-6	Sequence 6, Appl
36	162.5	12.3	231	4	US-08-543-246B-23	Sequence 23, Appl
37	158.5	12.0	134	4	US-08-543-246B-20	Sequence 20, Appl
38	158.5	12.0	216	4	US-08-543-246B-9	Sequence 9, Appl
39	158.5	12.0	216	4	US-08-543-246B-24	Sequence 24, Appl
40	154.5	11.7	199	5	PCT-US93-10418-2	Sequence 2, Appl
41	154	11.7	115	3	US-08-722-126A-8	Sequence 8, Appl
42	154	11.7	115	5	PCT-US95-04258-8	Sequence 8, Appl
43	150	11.4	1479	3	US-08-840-062-4	Sequence 4, Appl
44	149.5	11.3	233	1	US-08-690-095-8	Sequence 8, Appl
45	149.5	11.3	233	3	US-09-113-789-8	Sequence 8, Appl

#### ALIGNMENTS

RESULT 1  
US-09-055-095-3  
; Sequence 3, Application US/09055095  
; Patent No. 5945308  
GENERAL INFORMATION:  
APPLICANT: Tang, Y. Tom  
APPLICANT: Patterson, Chandra  
APPLICANT: Corley, Neil C.  
APPLICANT: Sathier, Susan  
TITLE OF INVENTION: HUMAN OXIDIZED LDL RECEPTOR  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESSES:  
ADDRESSER: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Dr.  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/055,095  
FILING DATE: Filed Herewith  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0500 US  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 650-855-0555  
TELEFAX: 650-845-4166  
INFORMATION FOR SEQ ID NO: 3:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 273 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
IMMEDIATE SOURCE:  
LIBRARY: GenBank  
CLONE: 1902984  
US-09-055-095-3  
Query Match 48.3%; Score 637; DB 2; Length 273;

Best Local Similarity 48.9%; Pred. No. 1.5e-49;  
Matches 134; Conservative 35; Mismatches 69; Indels 36; Gaps 6

QY	1	MTDQD-KKKPANDPEDDQSCCKKRESEORBLK	-----	-GKIDT- -	38
		: : :     :     :     :     :			
Db	1	MTPDLLKIQYAKDQDPEKSNKKAK	----	-GLOFLYSPMWMLAANTIGVLCGLGYITIMV	55
QY	39	-----TKRLDEKSKOEQELLMIOMIQ---	-BALORPANSSESEORBLKGKIDTLLTKLNE	90	
		:     :     :     :     :     :     :			
Db	56	LGMOLSOYSDLLTQEOALWTHQKKKLEPOLISAROOAEASOSESENELEKMETETLARKLNE	115		
QY	91	KSKEOEELLOKNONLOEALORPANSFGCPDMLMHKENCYLF-	-HGPGWKKENKPOSTOL	145	
		:     :     :     :     :     :     :			
Db	116	KSKEGEMELHROHNLNQETLKRVCANCSACPDWYIMHGENCELTFSSGSGFNMEKSOEKLSTL	175		
QY	150	GGQLLQINGADDLFTLLOAISHTTSPWIGLHRRKPGOPWIMLWNGTPINFLQFFKTRGVSL	205		
		:     :     :     :     :     :     :     :			
Db	176	DAKLKIKINSTADLLFIQOAIYSISFPFMGMGSRNPSPYMLMEDGSPIMPLHFLFRGAVS	235		
QY	210	QLYSSNCAYLQDGAVFAPENECILAFSTCOCKTN	243		
		:     :     :     :     :     :			
Db	236	QTYPSGTCATYORGAIVANECILAFSTCOCKKAN	269		

RESULT 2  
TIC-09-800

Sequence 6, Application US/0809494A  
 Patent No. 5963260  
 GENERAL INFORMATION:  
 APPLICANT: Sawamura, Tatsuya  
 APPLICANT: Masaki, Tomoo  
 TITLE OF INVENTION: Modified Low-Density Lipoprotein  
 TITLE OF INVENTION: Receptor  
 NUMBER OF SEQUENCES: 8  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: McAlilly Fisher Nissen Goldberg & Kiel  
 STREET: 261 Madison Avenue  
 CITY: New York  
 STATE: NY  
 COUNTRY: USA  
 ZIP: 10016-2391  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/809,494A  
 FILING DATE: 24-MAR-1997  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 6-321705  
 FILING DATE: 30-NOV-1994  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: JP 7-214206  
 FILING DATE: 31-JUL-1995  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Goldberg, Jules E  
 REGISTRATION NUMBER: 24408  
 REFERENCE/DOCKET NUMBER: JG-YY-4363PCT  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 212 986-4090  
 TELEFAX: 212 818-9479  
 INFORMATION FOR SEQ ID NO: 6:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 273 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 US-08-809-494A-6

Query Match 48.38; Score 637; DB 2; Length 273;

Best Local Similarity 48.9%; Pred. No. 1.5e-49;  
Matches 134; Conservative 35; Mismatches 69; Indels 36; Gaps 6

QY	1	MTFPD-KKKPANDPPDCKCKRRESSORELK-----KIDIT--	38
		: : : : :     : : : : :	
Db	1	MTFPDLKIQYKDDPDEKSNCKKAK-----GLQZLYSPMMCCLAATYLGVLCLGYVTIMV	55
		: : : : :     : : : : :	
QY	39	-----TRKLDKSKQEELLQMIQNLQ--EALQRAANSSEESORELKXIDTLYTKLNE	90
		: : : : :     : : : : :	
Db	56	LGMDLSQVSDLLTQEOANILTHOKKLLGQISARQAEASQESFENLEKEMITETLARKNE	115
		: : : : :     : : : : :	
QY	91	KSKROEELLQONLOEALRAANFSPCPQDMLWMEHCNYLF-HGSPGEXKRNQTCOSL	149
		: : : : :     : : : : :	
Db	116	KSKQDMELHHQNLQLELTKRVANCSAPCPQDMLWMEHCNYLFVSSGFSNMEKSOEKLSTL	175
		: : : : :     : : : : :	
QY	150	GGOLLOINGADDLFFILLOAISHTTPSPWIGLHRRKPPQAPMLWNGTFLNQFFKTRQVSL	209
		: : : : :     : : : : :	
Db	176	DAKLKINSTADLDFIQDAISYSFPPMWMGSRNRPSPYPMLEMGDSPLMHLFRVRGAVS	235
		: : : : :     : : : : :	
QY	210	QLYSSSCATYQDQGAFAENCILTAESICQKTN	243
		: : : : :     : : : : :	
Db	236	QTYPSGTCAYIQRGAVYAENCILTAESICQKTN	269
		: : : : :     : : : : :	

### RESULT 3

Sequence 6, APPLICATION US/09352302  
Patent No. 6197937  
GENERAL INFORMATION:  
APPLICANT: Sawamura, Tatsuya  
APPLICANT: Masaki, Tomoo  
TITLE OF INVENTION: Modified Low-Density Lipoprotein  
TITLE OF INVENTION: Receptor  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McAlail Fisher Nissen Goldberg & Kiel  
STREET: 261 Madison Avenue  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10016-2391  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/352,302  
FILING DATE: 12-JUL-1999  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-321705  
FILING DATE: 30-NOV-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 7-214206  
FILING DATE: 31-JUL-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Goldberg, Jules E  
REGISTRATION NUMBER: 24408  
REFERENCE/DOCKET NUMBER: JG-YY-4363PCT/D  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212 986-4090  
TELEFAX: 212 818-9479  
INFORMATION FOR SEQ ID NO.: 6:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 273 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein

Query Match	48.38; Score 637; DB 4; Length 273;
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Query Match 45.2%; Score 596; DB 2; Length 270;  
Best Local Similarity 44.6%; Pred. No. 7.1e-46;  
Matches 125; Conservative 39; Mismatches 70; Indels 46; Gaps 6;

QY 1 MTFDDKMPANDEPDOKSCGKPK-----EESQR 29  
DB 1 MTFDDP-KGMRDQDQKNGKTAKGVSSWRWYPAAVTLGVLGLLTVILLILOLSQ- 58  
QY 30 ELKGIKIDITTRKLEKSEKOEEL--OMIONLOEALORANSESEORLEKGIKIDITLTK 87  
DB 59 -----VSLIKKQOANTHODILEGQIL-----AQRRSEKSAQESQELKEMETLAKH 108  
QY 88 LNEKSKOEELLOKNOULOALORANFSGPCPODWIMHKENCYLF-HGPGMEKNQTC 146  
DB 109 LDEKSKLMEILHRONLNLQEVLEKAAVSGPCPODWIMHEENCYOFSSGSFMEKESQENC 168  
QY 147 QSLGGOLQINGADDLFTIIOAISHTTSPFVIGLHRRKPGCPWIMENGTPLNPFKTRG 206  
DB 169 LSLDAHLKINSTDELEFIQOMIAHSSPFVWGLSMRKNYSWIMEDGTPPLPHLFRIOG 228  
QY 207 VSLQVSSNCAYLQDGAFAENCILIAFSICOKRTNHLQ 246  
DB 229 AVSRMPSGTCAYIQRGTVFAENCILIAFSICOKKANILR 268

RESULT 6  
US-09-352-302-2  
; Sequence 2, Application US/09352302  
; Patent No. 6197937  
; GENERAL INFORMATION:  
; APPLICANT: Sawamura, Tatsuya  
; TITLE OF INVENTION: Modified Low-Density Lipoprotein  
; TITLE OF INVENTION: Receptor  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: McAlay Fisher Nissen Goldberg & Kiel  
; STREET: 261 Madison Avenue  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10016-2391  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/09/352,302  
; FILING DATE: 12-JUL-1999  
; CLASSIFICATION:  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 6-321705  
; FILING DATE: 30-NOV-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 7-214206  
; FILING DATE: 31-JUL-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Goldberg, Jules E  
; REGISTRATION NUMBER: 24408  
; REFERENCE/DOCKET NUMBER: JG-YV-4363PCT/D  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212 986-4090  
; TELEFAX: 212 818-9479  
; INFORMATION FOR SEQ ID NO: 2:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 270 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-09-352-302-2

Query Match 45.2%; Score 596; DB 4; Length 270;  
Best Local Similarity 44.6%; Pred. No. 7.1e-46;  
Matches 125; Conservative 39; Mismatches 70; Indels 46; Gaps 6;

QY 1 MTFDDKMPANDEPDOKSCGKPK-----EESQR 29  
DB 1 MTFDDP-KGMRDQDQKNGKTAKGVSSWRWYPAAVTLGVLGLLTVILLILOLSQ- 58  
QY 30 ELKGIKIDITTRKLEKSEKOEEL--OMIONLOEALORANSESEORLEKGIKIDITLTK 87  
DB 59 -----VSLIKKQOANTHODILEGQIL-----AQRRSEKSAQESQELKEMETLAKH 108  
QY 88 LNEKSKOEELLOKNOULOALORANFSGPCPODWIMHKENCYLF-HGPGMEKNQTC 146  
DB 109 LDEKSKLMEILHRONLNLQEVLEKAAVSGPCPODWIMHEENCYOFSSGSFMEKESQENC 168  
QY 147 QSLGGOLQINGADDLFTIIOAISHTTSPFVIGLHRRKPGCPWIMENGTPLNPFKTRG 206  
DB 169 LSLDAHLKINSTDELEFIQOMIAHSSPFVWGLSMRKNYSWIMEDGTPPLPHLFRIOG 228  
QY 207 VSLQVSSNCAYLQDGAFAENCILIAFSICOKRTNHLQ 246  
DB 229 AVSRMPSGTCAYIQRGTVFAENCILIAFSICOKKANILR 268

RESULT 7  
US-08-809-494A-4  
; Sequence 4, Application US/08809494A  
; Patent No. 5962260  
; GENERAL INFORMATION:  
; APPLICANT: Sawamura, Tatsuya  
; TITLE OF INVENTION: Modified Low-Density Lipoprotein  
; TITLE OF INVENTION: Receptor  
; NUMBER OF SEQUENCES: 8  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: McAlay Fisher Nissen Goldberg & Kiel  
; STREET: 261 Madison Avenue  
; CITY: New York  
; STATE: NY  
; COUNTRY: USA  
; ZIP: 10016-2391  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/809,494A  
; FILING DATE: 24-MAR-1997  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 6-321705  
; FILING DATE: 30-NOV-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: JP 7-214206  
; FILING DATE: 31-JUL-1995  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Goldberg, Jules E  
; REGISTRATION NUMBER: 24408  
; REFERENCE/DOCKET NUMBER: JG-YV-4363PCT  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 212 986-4090  
; TELEFAX: 212 818-9479  
; INFORMATION FOR SEQ ID NO: 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 273 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-809-494A-4

Query Match 45.1%; Score 594.5; DB 2; Length 273;  
Best Local Similarity 44.2%; Pred. No. 9.9e-46;  
Matches 125; Conservative 39; Mismatches 70; Indels 49; Gaps 6;

QY 1 MTFDDKMPANDEPDQKCGKKPK-----EE 26  
D 1 MTFDDKMPANDEPDQKCGKKPK-----EE 26  
QY 27 SORLEKGIIDITRRKLDKSKOEELL--OMIQNQLQALORANSSSORELKGIIDL 84  
D 1 MTFDDKMPANDEPDQKCGKKPK-----EE 26  
QY 60 SQ-----VSDIKKQOANTHEDILEGQIL-----AORSEKSAQESQKELKEMITL 108  
D 60 SQ-----VSDIKKQOANTHEDILEGQIL-----AORSEKSAQESQKELKEMITL 108  
QY 85 TLKLNKSKOEELLQKQNLQALORANSSGPPQDMLMKENCYL-F-HGPFGEKRN 143  
D 109 AHKLDKSKKLMELHRONLNQLQALORANSSGPPQDMLMKENCYL-F-HGPFGEKRN 143  
QY 144 QTCQSLQGLQIINGADLITFLQAIISHTSPFWIGLHKKRGQPLWENGTPPLNFQFPK 203  
D 169 ENCLSLDHLKINSTDELEFIQOMIAHSSFPFWMLSMKRPNYSWLMWEDGTPPLPHLFR 228  
QY 204 TRGVSLQYSSSNCAYLQDGAFAENCILITAFSIQOKKTNHLO 246  
D 229 IQGAVSRMTPSGTCAYIQRGIVFAENCILITAFSIQOKKANLRL 271

## RESULT 8

US-09-352-302-4  
Sequence 4, Application US/09352302  
Patent No. 6197937  
GENERAL INFORMATION:  
APPLICANT: Sawamura, Tatsuya  
APPLICANT: Masaki, Tomoo  
TITLE OF INVENTION: Modified Low-Density Lipoprotein  
NUMBER OF SEQUENCES: 8  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: McAlay Fisher Nissen Goldberg & Kiel  
STREET: 261 Madison Avenue  
CITY: New York  
STATE: NY  
COUNTRY: USA  
ZIP: 10016-2391  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/352.302  
FILING DATE: 12-JUL-1999  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 6-321705  
FILING DATE: 30-NOV-1994  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 7-214206  
FILING DATE: 31-JUL-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Goldberg, Jules E  
REGISTRATION NUMBER: 24408  
REFERENCE/DOCKET NUMBER: JG-YY-4363PCT/D  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 212 986-4090  
TELEFAX: 212 818-9479  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 273 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-09-352-302-4

Query Match 45.1%; Score 594.5; DB 4; Length 273;  
Best Local Similarity 44.2%; Pred. No. 9.9e-46;  
Matches 125; Conservative 39; Mismatches 70; Indels 49; Gaps 6;

QY 1 MTFDDKMPANDEPDQKCGKKPK-----EE 26  
D 1 MTFDDKMPANDEPDQKCGKKPK-----EE 26  
QY 27 SORLEKGIIDITRRKLDKSKOEELL--OMIQNQLQALORANSSSORELKGIIDL 84  
D 1 MTFDDKMPANDEPDQKCGKKPK-----EE 26  
QY 60 SQ-----VSDIKKQOANTHEDILEGQIL-----AORSEKSAQESQKELKEMITL 108  
D 60 SQ-----VSDIKKQOANTHEDILEGQIL-----AORSEKSAQESQKELKEMITL 108  
QY 85 TLKLNKSKOEELLQKQNLQALORANSSGPPQDMLMKENCYL-F-HGPFGEKRN 143  
D 109 AHKLDKSKKLMELHRONLNQLQALORANSSGPPQDMLMKENCYL-F-HGPFGEKRN 143  
QY 144 QTCQSLQGLQIINGADLITFLQAIISHTSPFWIGLHKKRGQPLWENGTPPLNFQFPK 203  
D 169 ENCLSLDHLKINSTDELEFIQOMIAHSSFPFWMLSMKRPNYSWLMWEDGTPPLPHLFR 228  
QY 204 TRGVSLQYSSSNCAYLQDGAFAENCILITAFSIQOKKTNHLO 246  
D 229 IQGAVSRMTPSGTCAYIQRGIVFAENCILITAFSIQOKKANLRL 271

## RESULT 9

US-08-688-342-1  
Sequence 1, Application US/08688342  
Patent No. 5871964  
GENERAL INFORMATION:  
APPLICANT: Au-Young, Janice  
APPLICANT: Cocks, Benjamin G.  
APPLICANT: Goli, Surya K.  
APPLICANT: Hillman, Jennifer L.  
TITLE OF INVENTION: NOVEL HUMAN C-TYPE LECTIN  
NUMBER OF SEQUENCES: 5  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Drive  
CITY: Palo Alto  
STATE: CA  
COUNTRY: US  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq Version 1.5  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/688.342  
FILING DATE: Filed Herewith  
ATTORNEY/AGENT INFORMATION:  
NAME: Billings, Lucy J.  
REGISTRATION NUMBER: 36,749  
REFERENCE/DOCKET NUMBER: PF-0095-1 CIP  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-855-0555  
TELEFAX: 415-845-4166  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 201 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: peptide  
IMMEDIATE SOURCE:  
LIBRARY: MMLRIDT01  
CLONE: 515847  
US-08-688-342-1

Query Match 19.0%; Score 251; DB 2; Length 201;  
Best Local Similarity 35.2%; Pred. No. 3.7e-15;



APPLICANT: Arizumi, Kiyoshi  
TITLE OF INVENTION: UNIQUE DENDRITIC CELL-ASSOCIATED C-TYPE  
TITLE OF INVENTION: LECTINS, DECTIN-1 AND DECTIN-2; COMPOSITIONS AND USES  
TITLE OF INVENTION: THEREOF  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: Texas  
COUNTRY: USA  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/772,440  
FILING DATE: CONCURRENTLY HERewith  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Parker, David L.  
REGISTRATION NUMBER: 32,165  
REFERENCE/DOCKET NUMBER: UTXD:493  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 512/418-3000  
TELEFAX: 512/474-7577  
INFORMATION FOR SEQ ID NO: 8:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 176 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
US-08-772-440-8

Query Match 17.5%; Score 231; DB 3; Length 176;  
Best Local Similarity 30.9%; Pred. No. 1.9e-13;  
Matches 50; Conservative 27; Mismatches 83; Indels 2; Gaps 2;

Qy 82 DTLTLKLNKSKOEELLQKNOQLQALQRAANFSGPCPDWLMHKENCYLF-HGPFGE 140  
Db 14 DNFLSRNKNHNPRESSLDEKVAPSKASQTGCFQSCLPMNIMHGKSCYLFSGNSWY 73  
Qy 141 KNRQTCQSLGGLQINGADLTFI-LQAIHTTSPFWIGLHRRKPGQWMLNENGPPLNF 199  
Db 74 GSKRHCQSLGAHLKIDNKEFEFTESQTSRIRNAFWIGLSRNOSEGEFWEDGSAFPP 133  
Qy 200 OFFKTRGVSLQYSSNCAYLQDGAFAVFAENCILIAFSICOKK 241  
Db 134 NSFQVRNTVPQESLHNCVWIGHSEVYNGICNTSSYSICEKE 175

RESULT 13  
US-08-772-440-2  
Sequence 2, Application US/08772440  
Patent No. 6046158  
GENERAL INFORMATION:  
APPLICANT: Arizumi, Kiyoshi  
APPLICANT: Takashima, Akira  
TITLE OF INVENTION: UNIQUE DENDRITIC CELL-ASSOCIATED C-TYPE  
TITLE OF INVENTION: LECTINS, DECTIN-1 AND DECTIN-2; COMPOSITIONS AND USES  
TITLE OF INVENTION: THEREOF  
NUMBER OF SEQUENCES: 42  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston  
STATE: Texas  
COUNTRY: USA  
ZIP: 77210

COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/772,440  
FILING DATE: CONCURRENTLY HERewith  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:  
NAME: Parker, David L.  
REGISTRATION NUMBER: 32,165  
REFERENCE/DOCKET NUMBER: UTXD:493  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 512/418-3000  
TELEFAX: 512/474-7577  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 244 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
US-08-772-440-2

Query Match 17.5%; Score 231; DB 3; Length 244;  
Best Local Similarity 30.9%; Pred. No. 3e-13;  
Matches 50; Conservative 27; Mismatches 83; Indels 2; Gaps 2;

Qy 82 DTLTLKLNKSKOEELLQKNOQLQALQRAANFSGPCPDWLMHKENCYLF-HGPFGE 140  
Db 82 DNFLSRNKNHNPRESSLDEKVAPSKASQTGCFQSCLPMNIMHGKSCYLFSGNSWY 141  
Qy 141 KNRQTCQSLGGLQINGADLTFI-LQAIHTTSPFWIGLHRRKPGQWMLNENGPPLNF 199  
Db 142 GSKRHCQSLGAHLKIDNKEFEFTESQTSRIRNAFWIGLSRNOSEGEFWEDGSAFPP 201  
Qy 200 OFFKTRGVSLQYSSNCAYLQDGAFAVFAENCILIAFSICOKK 241  
Db 202 NSFQVRNTVPQESLHNCVWIGHSEVYNGICNTSSYSICEKE 243

RESULT 14  
US-09-055-095-1  
Sequence 1, Application US/09055095  
Patent No. 5945308  
GENERAL INFORMATION:  
APPLICANT: Tang, Y. Tom  
APPLICANT: Patterson, Chandra  
APPLICANT: Corley, Neil C.  
APPLICANT: Sather, Susan  
TITLE OF INVENTION: HUMAN OXIDIZED LDL RECEPTOR  
NUMBER OF SEQUENCES: 4  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Incyte Pharmaceuticals, Inc.  
STREET: 3174 Porter Dr.  
CITY: Palo Alto  
STATE: CA  
COUNTRY: USA  
ZIP: 94304  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/055,095  
FILING DATE: Filed Herewith  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:





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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 19, 2002, 22:02:39 ; Search time 43.79 Seconds

(without alignments)  
541.997 Million cell updates/sec

Title: US-09-898-554-14

Perfect score: 1319

Sequence: 1 MTFDDKMKRANDEPDQKSCG.....ENCILIAFSICKKTNHLQI 247

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : PIR.71.\*

1: p1r1.\*  
2: p1r2.\*  
3: p1r3.\*  
4: p1r4.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1207	91.5	363	2 JE0111	lectin-like oxidiz
2	223	16.9	404	2 A46274	HIV gp120-binding
3	222.5	16.9	223	2 B46467	NKR-P1 protein hom
4	218.5	16.6	220	2 C46467	NKR-P1 protein hom
5	201.5	15.3	227	2 A46467	natural killer cel
6	190	14.4	309	1 S34198	IgE Fc receptor II
7	187.5	14.2	156	2 T28141	C type lectin, B 1
8	186	14.1	331	1 LNMSFR	IgE Fc receptor, I
9	174	13.2	223	2 A35917	NK-cell receptor, p
10	168.5	12.8	257	2 A50146	gene 17.5 protein
11	165.5	12.5	321	1 LNHDUR	IgE Fc receptor II
12	164.5	12.5	311	1 LNHDUR	asialoglycoprotein
13	163.5	12.4	550	2 A28166	Kufler cell recep
14	162.5	12.3	231	2 PR0374	natural killer cel
15	159	12.1	240	2 I54524	natural killer cel
16	159	12.1	1326	2 B56395	secretory phosphol
17	159	12.1	1465	2 A56395	secretory phosphol
18	158.5	12.0	216	2 PR0375	natural killer cel
19	156	11.8	266	2 I49050	Ly-49E-GE antigen
20	154.5	11.7	199	2 JH0822	lymphocyte early a
21	149.5	11.3	233	2 PR0372	natural killer cel
22	149	11.3	304	2 UX0209	lectin, galactose/
23	149	11.3	1479	2 T42710	mannose receptor,
24	148.5	11.3	225	2 I38700	hNKR-P1a protein -
25	142	10.8	1458	1 A49707	phospholipase A2 r
26	141.5	10.7	1463	2 A53210	phospholipase A2 r
27	137.5	10.4	1487	2 S48719	phospholipase A(2)
28	137	10.4	288	2 I49058	Ly49c - mouse
29	136.5	10.3	262	2 A45813	T-cell surface, gly

30	135	10.2	266	2 I49059	Ly49c - mouse
31	131.5	10.0	266	2 I49363	natural killer cel
32	131.5	10.0	306	2 A42230	lectin M-ASGP-BP p
33	131	9.9	354	2 A32331	B-cell differentia
34	130.5	9.9	262	2 I49361	natural killer cel
35	130.5	9.9	291	1 LNHDUR	hepatic lectin H1
36	130.5	9.9	1455	1 A48925	mannose receptor p
37	130	9.9	266	2 I49114	Ly49H - mouse
38	129	9.8	552	2 C96563	probable protein k
39	128.5	9.7	262	2 A30573	T-cell surface gly
40	128	9.7	321	2 T26152	hypothetical prote
41	127.5	9.7	237	2 JC7608	type II lectin-lik
42	127.5	9.7	1456	1 A36563	mannose receptor p
43	127	9.6	359	2 A46509	B cell differentia
44	126	9.6	167	1 WNVZP2	hepatic lectin hom
45	125.5	9.5	301	2 S13165	asialoglycoprotein

## ALIGNMENTS

RESULT 1

JE0111 Lectin-like oxidized LDL receptor - mouse

N:Alternate names: LDY-1

C:Species: Mus musculus (house mouse)

C>Date: 22-May-1998 #sequence\_revision 29-May-1998 #text\_change 07-May-1999

C:Accession: JE0111

R:Hoshikawa, H.; Sawamura, T.; Kakutani, M.; Aoyama, T.; Nakamura, T.; Masaki, T.

Biochem. Biophys. Res. Commun. 245, 841-846, 1998

A:Title: High affinity binding of oxidized LDL to mouse lectin-like oxidized LDL rece

A:Reference number: JE0111; MUID:98249801

A:Accession: JE0111

A:Molecule type: mRNA

A:Residues: 1-363 <HOS>

F:34-59/Domain: transmembrane #status predicted <TM>

Query Match 91.5% Score 1207; DB 2; Length 363;

Best Local Similarity 66.1%; Pred. No. 4, 1e-71;

Matches 240; Conservative 1; Mismatches 6; Indels 116; Gaps 1;

QY	1	MTFDDKMKRANDEPDQKSCGKKR	-----	24
DB	1	MTFDDKMKRANDEPDQKSCGKKR	-----	60
QY	25	-----	-----	24
DB	61	QVSDLLKQYANLTOODRILEGOMLAQCKAENTSOESKKELGKIDTLTQKINKEKQE	-----	120
QY	25	-----	-----	64
DB	121	ELLQKNQNLQELQRAANSEESQRELKGIIDTLTKLDEKSEDELLQNTQNLQELQ	-----	180
QY	65	RAANSEESQRELKGIIDTLTKLNEKSEQELQKNQNLQELQRAANSESPCPQDML	-----	124
DB	181	RAANSEESQRELKGIIDTLTKLNEKSEQELQKNQNLQELQRAANSEFGPCQDML	-----	240
QY	125	WIKENCYLFHGPGEKKNQTCOSLGGQLLIQNGADLTFIIQAISSHSPWIGLHRRK	-----	184
DB	241	WIKENCYLFHGPGEKKNQTCOSLGGQLLIQNGADLTFIIQAISSHSPWIGLHRRK	-----	300
QY	185	PCQPMWENGTPLNQFFETRGVSILQYSSNCAYLQDGAFAENCILIAFSICKKTNH	-----	244
DB	301	PCQPMWENGTPLNQFFETRGVSILQYSSNCAYLQDGAFAENCILIAFSICKKTNH	-----	360
QY	245	LQI 247	-----	247
DB	361	LQI 363	-----	363
RESULT	2	A46274	-----	2

HIV gp120-binding C-type lectin - human  
C:Species: Homo sapiens (man)  
C:Date: 21-Sep-1993 #sequence\_revision 18-Nov-1994 #text\_change 01-Dec-1995  
C:Accession: A46274  
R:Curts, B.M.; Scharnowske, S.; Watson, A.J.  
Proc. Natl. Acad. Sci. U.S.A. 89, 8356-8360, 1992  
A:Title: Sequence and expression of a membrane-associated C-type lectin that exhibits C  
A:Reference number: A46274; MUID:92390446  
A:Accession: A46274  
A:Status: preliminary  
A:Molecule type: nucleic acid  
A:Residues: 1-404 <CUR>  
A:Experimental source: placenta  
A:Note: sequence extracted from NCBI backbone (NCBIN:113134, NCBIP:113135)  
C:Superfamily: C-type lectin homology  
F:256-377/Domain: C-type lectin homology <LCH>

Query Match 16.9%; Score 223; DB 2; Length 404;  
Best Local Similarity 26.0%; Pred. No. 2, 1e-07;  
Matches 67; Conservative 54; Mismatches 107; Indels 30; Gaps 10;

Y 6 KMRPADEPQK-----CGKPREESQRELGKIDTIT--TRKLDKSK 47  
Db 129 RLKAAYGELEPKSKQEIYELTLKRAAYGELEPKSKQEIYELTLKRAAYGELEPKSK 188  
QY 48 EDELLQMIQNLQELQRAANSEESQ--RELKGIQTLTLKLNKSEDELLQKNQNL 105  
Db 189 -QOEIYQELRLKRAAYGELEPKSKQEIYELTLKRAAYGELEPKSK -QOEIYQELTQL 245  
QY 106 QELQRAANSGPCPDMLMKENCY-LFHGPGWCKNRQTCOSLGQQLQINCADLTFL 164  
Db 246 KAAVERLCH--PCPMWTFEGNCYFMSNSQRMWHDITACKEVGAQLVIVISAEQNF 302  
QY 165 ILQAISSHTSPFWIGLHRRKPGQPMLENGTPL--NFOEFTKGVSLQLYSSSCAYLQD 222  
Db 303 LQOSSRSNFTWGLSDLNQEGTWQVDSPLLPSTKQYWNNGEPNNV--GEEDCAFEFG 361  
QY 223 GAVFAENCILIAFSICOK 240  
Db 362 NGWMDCKNLAKFWICK 379

RESULT 3  
B46467  
NKR-P1 protein homolog - mouse  
C:Species: Mus musculus (house mouse)  
C:Date: 18-Jun-1993 #sequence\_revision 18-Nov-1994 #text\_change 24-Sep-1999  
C:Accession: B46467  
R:Giorda, R.; Trucco, M.  
Immunol. 147, 1701-1708, 1991  
A:Title: A family of genes selectively coexpressed in adherent lymphokine-activated k  
A:Reference number: A46467; MUID:91349596  
A:Accession: B46467  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-223 <GIO>  
A:Cross-references: GB:M77677; NID:q200060; PIDN:AAA39823.1; PID:q200061  
A:Experimental source: NK cells, C57BL/7  
A:Note: sequence extracted from NCBI backbone (NCBIN:52380, NCBIP:52381)  
C:Superfamily: natural killer cell receptor P1; C-type lectin homology  
C:Keywords: transmembrane protein  
F:94-210/Domain: C-type lectin homology <LCH>

Query Match 16.9%; Score 222.5; DB 2; Length 223;  
Best Local Similarity 32.1%; Pred. No. 1, 2e-07;  
Matches 50; Conservative 22; Mismatches 77; Indels 7; Gaps 3;

QY 90 EKSKQDELLQKNQNLQELQRAANSGPCPDMLMKENCY-LFHGPGWCKNRQTCOS 148  
Db 67 OKSSVQKICADVQENRHTHTDGSVNL--CPQDWLSHRDGCFNRYFQVSNWESQADCGR 124

QY 149 LGQQLQINCADLTFLQAISSHTSPFWIGLHRRKPGQPMLENGTPLNFOEFTKGVCS 208  
Db 125 KGAITLLIQDEELRFLDLSIKENYNSFWIGLHRRKPGQPMLENGTPLNFOEFTKGVCS 184  
QY 209 LQIYSSNCAYLQDGAFAENCILIAFSICOKNNH 244  
Db 185 ----ENGSCASISGDKVTSQSTDNRMWICKQELNH 216

RESULT 4  
C46467  
NKR-P1 protein homolog gene-40 - mouse  
N:Alternate names: natural killer cell activation molecule; NK1.1 alloantigen  
C:Species: Mus musculus (house mouse)  
C:Date: 18-Jun-1993 #sequence\_revision 18-Nov-1994 #text\_change 24-Sep-1999  
C:Accession: C46467; A46499  
R:Giorda, R.; Trucco, M.  
Immunol. 147, 1701-1708, 1991  
A:Title: A family of genes selectively coexpressed in adherent lymphokine-activated k  
A:Reference number: A46467; MUID:91349596  
A:Accession: C46467  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-220 <GIO>  
A:Cross-references: GB:M77678; NID:q200062; PIDN:AAA39824.1; PID:q200063  
A:Experimental source: NK cells, C57BL/7  
A:Note: sequence extracted from NCBI backbone (NCBIN:52382, NCBIP:52383)  
R:Ryan, J.C.; Turk, J.; Nleml, E.C.; Yokoyama, W.M.; Seaman, W.E.  
J. Immunol. 149, 1631-1635, 1992  
A:Title: Molecular cloning of the NK1.1 antigen, a member of the NKR-P1 family of nat  
A:Reference number: A46499; MUID:92373004  
A:Accession: A46499  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-86, 90-220 <RYA>  
A:Cross-references: GB:S43141; NID:q254094; PIDN:AAB22979.1; PID:q254095  
A:Experimental source: C57BL/6J NK cells  
A:Note: sequence extracted from NCBI backbone (NCBIN:111622, NCBIP:111624)  
C:Superfamily: natural killer cell receptor P1; C-type lectin homology  
C:Keywords: transmembrane protein  
F:91-207/Domain: C-type lectin homology <LCH>

Query Match 16.6%; Score 218.5; DB 2; Length 220;  
Best Local Similarity 33.1%; Pred. No. 2, 2e-07;  
Matches 50; Conservative 19; Mismatches 65; Indels 17; Gaps 3;

QY 95 OEELLQKNQNLQELQRAANSGPCPDMLMKENCY-LFHGPGWCKNRQTCOSLGQQL 153  
Db 79 QENLQKTTVNDL-----CPQDWLHRRKCFHVSQVSNWESQADCGRKGATL 126  
QY 154 LQINGADLTFLQAISSHTSPFWIGLHRRKPGQPMLENGTPLNFOEFTKGVSLQLYS 213  
Db 127 LLIQDQELRFLDLSIKENYNSFWIGLHRRKPGQPMLENGTPLNFOEFTKGVSLQLYS 182  
QY 214 SSSNCAYLQDGAFAENCILIAFSICOKNNH 244  
Db 183 NGSCASISGDKVTSQSTDNRMWICKQELNH 213

RESULT 5  
A46467  
natural killer cell receptor P1 - mouse  
N:Alternate names: NKR-P1 protein  
C:Species: Mus musculus (house mouse)  
C:Date: 18-Jun-1993 #sequence\_revision 19-Feb-1999 #text\_change 05-May-2000  
C:Accession: A46467; A46502; A46456  
R:Giorda, R.; Trucco, M.  
Immunol. 147, 1701-1708, 1991  
A:Title: A family of genes selectively coexpressed in adherent lymphokine-activated k  
A:Reference number: A46467; MUID:91349596  
A:Accession: A46467  
A:Molecule type: mRNA

A:Residues: 'MHLICT', 1-227 <GIO>  
A:Cross-references: GB:M77676; NID:g200058  
A:Experimental source: A-IAP cells, C57BL  
A:Note: sequence extracted from NCBI backbone (NCBIN:52378, NCBI:P:52379); the sequence  
R:Giorde, R., Weisberg, E.P., ID, T.K., Trucco, M.  
J:Immunol. 149, 1957-1963, 1992  
A:Title: Genomic structure and strain-specific expression of the natural killer cell re  
A:Reference number: A46502; MUID:92388663  
A:Accession: A46502  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-109, 'H', 111-181, 'D', 183-227 <G12>  
A:Cross-references: GB:X64716; NID:g53395; PIDN:CAA5971.1; PID:g817989  
A:Experimental source: BALB/c 3T3 fibroblastoid cell line  
A:Note: sequence extracted from NCBI backbone (NCBIN:113037, NCBIN:113063, NCBIN:113072,  
R:Yokoyama, W.M., Ryan, J.C., Hunter, J.J., Smith, H.R., Stark, M., Seaman, W.E.  
J:Immunol. 147, 3228-3236, 1991  
A:Title: cDNA cloning of mouse NK-RP1 and genetic linkage with LY-49. Identification of  
A:Reference number: A46456; MUID:92013158  
A:Accession: A46456  
A:Molecule type: mRNA  
A:Residues: 1-38, 'L', 40-227 <YOK>  
A:Cross-references: GB:M7753; NID:g198569; PIDN:AAA39366.1; PID:g198570  
A:Note: sequence extracted from NCBI backbone (NCBIN:60429, NCBI:P:60431)  
C:Superfamily: natural killer cell receptor P1; C-type lectin homology  
F:94-210/Domain: C-type lectin homology <LCH>

Query Match 15.3%; Score 201.5; DB 2; Length 227;  
Best Local Similarity 32.2%; Pred. No. 2.8e-06;  
Matches 46; Conservative 21; Mismatches 69; Indels 7; Gaps 3;

OY 105 LOEALQRRANFSG--PCQDMLMHEKNCY-LFHGFGMEKNQTCQSLGGOLQINGADD 161  
DB 78 IQENLNKTTDCSAKIEQDMLSHDKCFHVSQVNTBEGLVDCDGGATMLIQDDE 137  
OY 162 LFTLLQATISHTSPFWIGLHRRKPGQPMWENGPLNFQFKTRGVSLQLYSSNCAYLQ 221  
DB 138 LRFLLDSIKERYNSFWIGLRYTLPLDMNWKWINGSTLNSDVLKITDGT----ENDSCAIS 193  
OY 222 DGAVFAENCILIAFSIOCKRTNH 244  
DB 194 GDKVTFESCNSDMRWICKELEYH 216

## RESULT 6

334198  
A:Fc receptor II, low-affinity - rat  
N:Alternate names: CD23; lymphocyte IGE receptor  
C:Species: Rattus norvegicus (Norway rat)  
C:Date: 06-Jan-1995 #sequence\_revision 06-Jan-1995 #text\_change 22-Jun-1999  
R:Flores-Romo, L., Sheld, J., Humbert, Y., Graber, P., Aubry, J.P., Gauchat, J.F.: Ayal  
submitted to the EMBL Data Library, June 1993  
A:Description: Inhibition of an in vivo antigen-specific IGE response by antibodies to C  
A:Reference number: S34198  
A:Accession: S34198  
A:Molecule type: mRNA  
A:Residues: 1-309 <FLO>  
A:Cross-references: EMBL:X73579; NID:g313672; PIDN:CAA51981.1; PID:g313673  
C:Superfamily: IGE receptor II; C-type lectin homology  
C:Keywords: B-cell; glycoprotein; immunoglobulin receptor; macrophage; tandem repeat; tr  
F:1-25/Domain: intracellular #status predicted <INT>  
F:14-22/Region: stop-transfer sequence  
F:24-46/Domain: transmembrane #status predicted <TM>  
F:47-309/Domain: extracellular #status predicted <EXT>  
F:126-309/Product: soluble IGE-binding factor (29K) #status predicted <IGI>  
F:149-309/Product: soluble IGE-binding factor (25K-27K) #status predicted <BEFI>  
F:164-283/Domain: C-type lectin homology <LCH>  
F:192-283,260-274/Disulfide bonds: #status predicted

Query Match 14.4%; Score 190; DB 1; Length 309;

Best Local Similarity 24.8%; Pred. No. 2.2e-05;  
Matches 69; Conservative 42; Mismatches 85; Indels 82; Gaps 11;  
OY 13 EPPDKSCGKKKPREESORELJKIDITTRKL-----DKSKEO-----ELLQMI 56  
DB 11 EPPRRRC-CCARGTOLVGLTVMVLLALLLHWETKSLKQJADAATQNALDMS 69  
OY 57 QNLQALORANSSSESORELKGIPTLTKLNEKSK-----QOEELQKNQMLQBAL 109  
DB 70 QNLDEL-----QAEQKQMSQDSQSLQNLNELQEDLQINKSQNSLSQNLNTLQEDL 121  
OY 110 -----QRANFS-----GPCQDMLMHEKNCYL-FHG 135  
DB 122 VNVKSGQINERKRAASDSLEKLEEVAKLWELTMSKGTACNCPKDWLHFOCKCYFEG 181  
OY 136 PCGMEKNQTCQSLGOLQINGADDLFTLLQATISHTSPFWIGLHRRKPGQPMWENG 195  
DB 182 SKWQIAQFTCSDLGRVLSHSQKEQDPLQKHKKES--WIGLQDLNMEGEFVWPGDS 239  
OY 196 PLNFQFKTRGVSLQLYSSNCAYLQDGAFAENCIL 233  
DB 240 PVG-----YSNMNPGEPNNGQ-GEDEVMA 263

## RESULT 7

728141  
C type lectin, B locus - chicken  
C:Species: Gallus gallus (chicken)  
C:Date: 15-Oct-1999 #sequence\_revision 15-Oct-1999 #text\_change 15-Oct-1999  
C:Accession: T28141  
R:Milne, S.; Kaufman, J.; Beck, S.  
submitted to the EMBL Data Library, May 1998  
A:Description: DNA sequencing and analysis of the chicken major histocompatibility co  
A:Reference number: 220475  
A:Accession: T28141  
A:Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-156 <ML>  
A:Cross-references: EMBL:AL023516; NID:e1292539; PID:e1292545; PIDN:CAA18961.1  
A:Experimental source: clone CB12  
C:Genetics: Blec  
A:Gene: Blec  
A:Map position: 16  
A:Introns: 17/1; 74/3; 110/2

Query Match 14.2%; Score 187.5; DB 2; Length 156;  
Best Local Similarity 30.9%; Pred. No. 1.5e-05;  
Matches 38; Conservative 20; Mismatches 54; Indels 11; Gaps 3;

OY 119 CPQDMLMHEKNCYL-FHGFGMEKNQTCQSLGOLQINGADDLFTLLQATISHTSPFW 177  
DB 30 CPFDWIGRGKRYTSEDESNTSSONNCASALGASLANFDSADLSFTWR--HKSSPPW 87  
OY 178 IGLHRRKPGQPMWENGPLNFQFKTRGVSLQLYSSNCAYLQDGAFAENCILIAFSI 237  
DB 88 VGLSREGKHPWEWNRPSLSLFL-----QVGGDGLCAVLGAGLSSHCSTRRMVY 139  
OY 238 COK 240  
DB 140 CTK 142

## RESULT 8

LNMSR  
IGE Fc receptor, low-affinity - mouse  
N:Alternate names: Blast-2; CD23; Fc-epsilon-RII; lymphocyte IGE receptor  
C:Species: Mus musculus (house mouse)  
C:Date: 12-Feb-1993 #sequence\_revision 28-Oct-1994 #text\_change 22-Jun-1999  
C:Accession: A43518; A33840  
R:Gollnick, S.O., Tronstine, M.L., Yamashita, L.C.; Kehry, M.R.; Moore, K.W.  
J:Immunol. 144, 1974-1982, 1990  
A:Title: Isolation, characterization, and expression of cDNA clones encoding the mous



A:Molecule type: DNA  
A:Residues: 157-284 <SUT>  
A:Cross-references: GB:X06049; NID:g31316  
A:Note: all exon sequences were determined but the complete sequence is not shown  
R:Matsumi, M.; Nunez, R.; Sachl, Y.; Lynch, R.G.; Yodoi, J.  
FEBS Lett. 335, 51-56, 1993  
A:Title: Alternative transcripts of the human CD23/Fc-epsilon-RII. A possible novel mechanism  
A:Reference number: S39442; MUID:94063078  
A:Accession: S39442  
A:Molecule type: DNA  
A:Residues: 1-7, 'D', 47-50 <MAS1>  
A:Experimental source: splice form 'a'  
A:Accession: S39443  
A:Molecule type: DNA  
A:Residues: 'NMPSOD', 47-50 <MAS2>  
A:Experimental source: splice form 'b'  
R:Ludin, C.; Holstetter, H.; Sarfati, M.; Levy, C.A.; Suter, U.; Alaimo, D.; Kilcherr, E.MBO J. 6, 109-114, 1987  
A:Title: Cloning and expression of the cDNA coding for a human lymphocyte IgE receptor.  
A:Reference number: A26164; MUID:87218454  
A:Accession: A26164  
A:Molecule type: mRNA  
A:Residues: 1-268, 'T', 270-321 <LUD>  
A:Cross-references: GB:X04772; NID:g34002; PIDN:CAA28465.1; PID:g34003  
A:Note: the codon given for 269-Asn (ACC) is inconsistent with the authors' translation  
A:Note: part of this sequence, including the amino end of soluble forms of the protein,  
R:Ikuta, K.; Takami, M.; Kim, C.W.; Honjo, T.; Miyoshi, T.; Tagaya, Y.; Kawabe, T.; Yodoi Proc. Natl. Acad. Sci. U.S.A. 84, 819-823, 1987  
A:Title: Human lymphocyte Fc receptor for IgE: sequence homology of its cloned cDNA with  
A:Reference number: A26589; MUID:87118255  
A:Accession: A26589  
A:Molecule type: mRNA  
A:Residues: 1-321 <IKU>  
A:Cross-references: GB:M15059; NID:g182447; PIDN:MAA52434.1; PID:g182448  
A:Note: part of this sequence, including the amino end of soluble forms of the protein,  
R:Yokota, A.; Kikuchi, H.; Tanaka, T.; Sato, R.; Barsumian, E.L.; Suenmura, M.; Kishimoto Cell 55, 611-618, 1988  
A:Title: Two species of human Fc-epsilon receptor II (Fc-epsilon-RII/CD23): tissue-specific  
A:Reference number: A31924; MUID:89028672  
A:Accession: A31924  
A:Molecule type: mRNA  
A:Residues: 'NMPSQ', 8-14 <YOK>  
A:Cross-references: GB:M2562; NID:g182444  
A:Experimental source: splice form IIB  
R:Letellier, M.; Sarfati, M.; Delespesse, G.  
Mol. Immunol. 26, 1105-1112, 1989  
A:Title: Mechanisms of formation of IgE-binding factors (soluble CD23)-I. Fc epsilon R II  
A:Reference number: JLO132; MUID:90220658  
A:Accession: JLO132  
A:Molecule type: protein  
A:Residues: 1-321 <LET>  
A:Experimental source: lymphoblastoid B cell line  
R:Rose, K.; Turcatti, G.; Graber, P.; Pochon, S.; Regamey, P.O.; Jansen, K.U.; Magneat, Biochem. J. 286, 819-824, 1992  
A:Title: Partial characterization of natural and recombinant human soluble CD23.  
A:Reference number: S29107; MUID:93038513  
A:Accession: S29107  
A:Molecule type: protein  
A:Residues: 152-166, 173-179, 189-212, 230-263, 268-306 <ROS>  
R:Padali, E.A.; Helm, B.A.  
submitted to the Brookhaven Protein Data Bank, June 1993  
A:Reference number: A51791; PDB:1HUI  
A:Contents: annotation; conformation by theoretical model, residues 173-285  
R:Bejorath, J.  
submitted to the Brookhaven Protein Data Bank, November 1995  
A:Reference number: A65963; PDB:1KUE  
A:Contents: annotation; conformation by theoretical model, residues 173-285  
C:Comment: The sequence of the splice form 'a' is shown.  
C:Comment: This receptor for the Fc portion of IgE is expressed in various hematopoietic cells.  
C:Comment: Splice form 'a' is expressed constitutively in B-cells; 'b' is expressed in other cells.  
C:Comment: Soluble IgE-binding factors are produced by proteolytic cleavage of IgE Fc region  
C:Genetics:

A:Gene: GDB:FCER2; FCE2  
A:Cross-references: GDB:118888; OMIM:151445  
A:Map position: 19p13.3-19p13.3  
A:Introns: 8/1, 46/1, 64/1, 85/1, 106/1, 127/1, 157/1, 207/3, 243/2  
C:Superfamily: IgE receptor II; C-type lectin homology  
C:Keywords: alternative splicing; B-cell; glycoprotein; immunoglobulin receptor; macrophage; 'NMPSOD', 47-321/Product; IgE Fc receptor II, splice form b' #status predicted <SFB>  
F: 'NMPSQ', 8-321/Product; IgE Fc receptor II, splice form a' #status predicted <SFA>  
F:1-321/Product; IgE Fc receptor II, splice form a' #status predicted <SFA>  
F:1-23/Domain: Intracellular #status predicted <INT>  
F:1-7, 'D', 47-321/Product; IgE Fc receptor II, splice form 'a' #status predicted <SFA>  
F:14-20/Region: stop-transfer sequence  
F:22-45/Domain: transmembrane #status predicted <TM>  
F:46-321/Domain: extracellular #status predicted <EXT>  
F:64-84/Region: 21-residue repeat  
F:81-321/Product: soluble IgE-binding factor (37K) #status predicted <IGE>  
F:85-105/Region: 21-residue repeat  
F:106-126/Region: 21-residue repeat  
F:102-321/Product: soluble IgE-binding factor (33K) #status predicted <IGB>  
F:125-321/Product: soluble IgE-binding factor (29K) #status predicted <IGT>  
F:148-321/Product: soluble IgE-binding factor (25-27K), long form #status experimental  
F:150-321/Product: soluble IgE-binding factor (25-27K), short form #status experimental  
F:163-282/Domain: C-type lectin homology <LCH>  
F:63/Binding site: carbohydrate (Asn) (covalent) #status predicted  
F:147-148/Cleavage site: Lys-Ileu (unidentified proteinase) #status experimental  
F:149-150/Cleavage site: Arg-Met (unidentified proteinase) #status experimental  
F:191-282, 259-273/Disulfide bonds: #status experimental

Query Match 12.5%; Score 165.5; DB 1; Length 321;  
Best Local Similarity 28.7%; Pred. No. 0.00087;  
Matches 51; Conservative 33; Mismatches 75; Indels 19; Gaps 7;

QY 28 QRELKGIKIDITTRKDEKSEDEEL---LQNTQNLQALQRAANSSEBSQELKGIKIDT 83  
DB 78 QMAQKSSQSTQSQEDELRAEQRLKSDLELSMWL-NQLQ--ADLSFKSQELNER--- 131  
QY 84 LFLKLNKSEKQDEELQNNQNLQALQRAANF--SSCPQDDMLMHKENCYLE-HGPFGEK 141  
DB 132 -----NEASDLLERLREETTKLMELQVSSGVCVCTCPKTNFQKCYTEKGRKQWVH 186  
QY 142 NRQTCOSLQGLQINGADLFLIQAISHTSPFWIGLHRRKPPQPMLENGTFLNF 199  
DB 187 ARVACDDMDGQVSIHSPEDQFLRKHSHTGS--WIGLRNLDLGEFIWVGSHVDY 242

## RESULT 12

LNH02A  
asialoglycoprotein receptor H2a - human  
N:Alternate names: hepatic lectin H2a  
N:Contents: ASGPR; asialoglycoprotein receptor H2a; asialoglycoprotein receptor H2b  
C:Species: Homo sapiens (man)  
C:Date: 31-Mar-1988 #sequence revision 31-Mar-1988 #text change 10-Dec-1999  
C:Accession: A25179; A39100; B39100; I37995; A49466; B49466; S14525  
R:Spies, M.; Lodish, H.F.  
Proc. Natl. Acad. Sci. U.S.A. 82, 6465-6469, 1985  
A:Title: Sequence of a second human asialoglycoprotein receptor: conservation of two  
A:Reference number: A25179; MUID:86016723  
A:Accession: A25179  
A:Molecule type: mRNA  
A:Residues: 1-311 <SPI>  
A:Cross-references: GB:M11025; NID:g179080; PIDN:MAA59519.1; PID:g179081  
R:Ledgerkremer, G.Z.; Lodish, H.F.  
J. Biol. Chem. 266, 1237-1244, 1991  
A:Title: An alternatively spliced minlexon alters the subcellular fate of the human a  
A:Reference number: A39100; MUID:91093236  
A:Accession: A39100  
A:Molecule type: DNA; mRNA  
A:Residues: 69-99 <LED>  
A:Cross-references: GB:M38420; NID:g184395  
A:Accession: B39100  
A:Molecule type: DNA; mRNA





```

OY 66 AANSEESQRELKJCKIDPLTLKNEKSEKQEBELLÖKKÖNQNLQALQBRANSGCCPDWL 125
Db 64 LLPPEKFLTAVALDLCIVLDAVLKTYVLPELEONSSPNRTQAKRHCGCPEWIT 123
OY 126 HKENCYLTFHGPGF-----WEKNRQTCSLGOLLQINGADLPLFLQAIHTSPWIGL 180
Db 124 YSNCTY----TGERRTWESBLACTSKNSLSLIDNEEBKFLASILPSS----WIGV 175
OY 181 HRRKPGQVMEWENGTPLNFOFFKTRGVSQDLYSSNCAYLQDGAFAEMC 230
Db 176 FRNSHHBPWTYINGLAKRHKTKSDNAL-----KCAVLQVNRKLSAQC 219

```

RESULT 15

natural killer cell receptor group 2-C, splice form 2 - human  
 C:Species: Homo sapiens (man)  
 C:Date: 07-Jun-1996 #sequence\_revision 07-Jun-1996 #text\_change 19-May-2000  
 C:Accession: 154524  
 R:Adamkiewicz, T.V.; McSherry, C.; Bach, F.H.; Houchins, J.P.  
 Immunogenetics 39, 218, 1994  
 A:Title: Natural killer lectin-like receptors have divergent carboxy-termini, distinct  
 A:Reference number: 154524; MUID:94102823  
 A:Accession: 154524  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-240 <RES>  
 A:Cross-references: GB:LI4542; NID:g9292360; PIDN:AAA16833.1; PID:g9292361  
 C:Genetics:  
 A:Gene: GDB:KLRG2; NMG2-C  
 A:Cross-references: GDB:9787095  
 A:Map position: 1P13/1P13  
 A:Superfamily: natural killer cell receptor P1; C-type lectin homology

Query Match	12.1%	Score 159	DB 2	Length 240
Best Local Similarity	22.9%	Pred. No. 0.0017		
Matches 53	Conservative 40	Mismatches 98	Indels 40	Gaps 8

[illegible]

Search completed: August 19, 2002, 22:59:09  
Job time: 3390 sec

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FT DISULFID 122 210 BY SIMILARITY.  
 FT DISULFID 189 202 BY SIMILARITY.  
 FT CARBOHYD 81 81 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 169 169 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 223 AA; 25157 MW; 8D04C11DEBAB9C56 CRC64;

Query Match 16.9%; Score 222.5; DB 1; Length 223;  
 Best Local Similarity 32.1%; Pred. No. 4.3e-08;  
 Matches 50; Conservative 22; Mismatches 77; Indels 7; Gaps 3;

QY 90 EKSFEQELQKNNLOEALQANFSGPCQPDMLMKENY-LFHGPFGEKRNQTCOS 148  
 DB 67 QKSSVQKICADVQENRHTTDCSYNLE--CPQDWLSHRDKCFRVOYSNTWEGQADCGR 124  
 QY 149 LGGQLQINGADDTLFIQAIHTTSPFWIGLHRRKPGQPMWENCTPLNFQFKTRGVS 208  
 DB 125 KGATLLIQDEELRFLDISEKEKYNFVIGLRFPLDMNKKWINGTTFNSDVKITGDT 184  
 QY 209 LQLYSSNCAYLDGAVFAENCILIAFSICOKKTNH 244  
 B 185 -----ENGSCASISGDKVTSECSFDNRWICOKELNH 216

RESULT 2  
 NK14\_MOUSE  
 ID NK14\_MOUSE STANDARD; PRT; 220 AA.  
 AC P27814;  
 DT 01-AUG-1992 (Rel. 23, Created)  
 DT 01-AUG-1992 (Rel. 23, Last sequence update)  
 DT 15-JUL-1999 (Rel. 38, Last annotation update)  
 DE Natural killer cell surface protein PI-40 (NKR-PI 40) (NKR-PI.9).  
 GN LY55C OR LY55-C.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OC NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91349596; PubMed=1880421;  
 RA Giorda R., Trucco M.;  
 RT "Mouse NKR-PI. A family of genes selectively coexpressed in adherent lymphokine-activated killer cells.";  
 RT J. Immunol. 147:1701-1708(1991).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=C57BL/6J;  
 RX MEDLINE=92373004; PubMed=1506685;  
 RA Ryan J.C., Turck J., Niemi E.C., Yokoyama W.M., Seaman W.E.;  
 RT "Molecular cloning of the NK1.1 antigen, a member of the NKR-PI family of natural killer cell activation molecules.";  
 RT J. Immunol. 149:1631-1635(1992).  
 RL J. Immunol. 149:1631-1635(1992).  
 CC -1- FUNCTION: MAY FUNCTION AS SIGNAL-TRANSMITTING RECEPTOR.  
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein.  
 CC -1- TISSUE SPECIFICITY: NATURAL KILLER CELLS.  
 CC -1- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC EMBL: M77628; AAA39824.1; -  
 DR PIR: C46467; C46467.  
 DR SWISS-2DPAGE: P27814; MOUSE.  
 DR MGI: MGI:107538; LY55C.  
 DR InterPro: IPR001304; lectin.c.  
 DR Pfam: PF00059; lectin.c.1.  
 DR SMART: SM00034; CLECT; 1.

DR PROSITE: PS00615; C-TYPE LECTIN\_1; FALSE\_NEG.  
 DR PROSITE: PS50041; C-TYPE LECTIN\_2; 1.  
 KW Glycoprotein; Antigen; Transmembrane; Signal-anchor; Lectin.  
 FT DOMAIN 1 42 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 43 62 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN) (POTENTIAL).  
 FT DOMAIN 63 220 EXTRACELLULAR (POTENTIAL).  
 FT DOMAIN 90 212 C-TYPE LECTIN (LONG FORM).  
 FT DISULFID 91 102 BY SIMILARITY.  
 FT DISULFID 119 207 BY SIMILARITY.  
 FT DISULFID 186 199 BY SIMILARITY.  
 FT CARBOHYD 83 83 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 166 166 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 183 183 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 220 AA; 24771 MW; 8A160B1DEDA6398F CRC64;

Query Match 16.6%; Score 218.5; DB 1; Length 220;  
 Best Local Similarity 33.1%; Pred. No. 7.7e-08;  
 Matches 50; Conservative 19; Mismatches 65; Indels 17; Gaps 3;

QY 95 QEELQKNNLOEALQANFSGPCQPDMLMKENY-LFHGPFGEKRNQTCOSLGOL 153  
 DB 79 QENLKTNYNE-----CPQDWLSHRDKCFRVOYSNTWEGQADCGKCATL 126  
 QY 154 LQINGADDTLFIQAIHTTSPFWIGLHRRKPGQPMWENCTPLNFQFKTRGVSLOLYS 213  
 DB 127 LLIQDEELRFLDISEKEKYNFVIGLRFPLDMNKKWINGTTFNSDVKITGVT-----E 182  
 QY 214 SSNCAIYLDGAVFAENCILIAFSICOKKTNH 244  
 DB 183 NGSCASISGDKVTSECSFDNRWICOKELNH 213

RESULT 3  
 NK11\_MOUSE  
 ID NK11\_MOUSE STANDARD; PRT; 227 AA.  
 AC P27811;  
 DT 01-AUG-1992 (Rel. 23, Created)  
 DT 01-AUG-1992 (Rel. 23, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Natural killer cell surface protein PI-2 (NKR-PI 2) (NKR-PI.7).  
 GN LY55A OR LY55.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OC NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=91349596; PubMed=1880421;  
 RA Giorda R., Trucco M.;  
 RT "Mouse NKR-PI. A family of genes selectively coexpressed in adherent lymphokine-activated killer cells.";  
 RT J. Immunol. 147:1701-1708(1991).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=92031358; PubMed=1680927;  
 RA Yokoyama W.M., Ryan J.C., Hunter J.J., Smith H.R.C., Stark M., Seaman W.E.;  
 RT "CDNA cloning of mouse NKR-PI and genetic linkage with LY-49. Identification of a natural killer cell gene complex on mouse chromosome 6.";  
 RT J. Immunol. 147:3229-3236(1991).  
 RL J. Immunol. 147:3229-3236(1991).  
 CC -1- FUNCTION: MAY FUNCTION AS SIGNAL-TRANSMITTING RECEPTOR.  
 CC -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED.  
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein.  
 CC -1- TISSUE SPECIFICITY: NATURAL KILLER CELLS.  
 CC -1- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.  
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CC -----

DR EMBL; M7676; AAA39822.1; -;  
 DR EMBL; M7753; AAA3936.1; -;  
 DR MGI; MGI:107540; Ly55a.  
 DR InterPro: IPR001304; lectin\_c.  
 DR Pfam: PF00059; lectin\_c.1.  
 DR SMART: SM00034; CLECT; 1.  
 DR PROSITE; PS00615; C-TYPE\_LLECTIN.1; FALSE\_NEG.  
 DR PROSITE; PS50041; C-TYPE\_LLECTIN.2; 1.  
 DR Glycoprotein; Antigen; Transmembrane; Signal-anchor; Lectin.  
 FT DOMAIN 1 42 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 43 62 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)  
 FT (POTENTIAL).  
 FT DOMAIN 63 227 EXTRACELLULAR (POTENTIAL).  
 FT DOMAIN 93 212 C-TYPE LECTIN (LONG FORM).  
 FT DISULFID 94 105 BY SIMILARITY.  
 FT DISULFID 122 210 BY SIMILARITY.  
 FT DISULFID 189 202 BY SIMILARITY.  
 FT CARBOHYD 83 83 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 169 169 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CONFLICT 39 39 S -> L (IN REF. 2).  
 SQ SEQUENCE 227 AA; 25689 MM; 0599A2587DF0B615 CRC64;

Query Match 15.3%; Score 201.5; DB 1; Length 227;  
 Best Local Similarity 32.2%; Pred. No. 1e-06;  
 Matches 46; Conservative 21; Mismatches 69; Indels 7; Gaps 3;

OY 105 LOEALORANFSG--PCPODWIMHKNKY-LFHGFGEKKNQTOGSGCOLQINGADD 161  
 DB 78 IQENINKTTDSAKLECPDWLSHDKCFHVSQVNTWBEGLVDCGKATMLTQDOPE 137  
 OY 162 LTFILQAISSHSTSPWIGLHRRKPGOPWLMNGPPLNFQFFTRGVSLQLYSSNCAYLQ 221  
 DB 138 LRFLLDSIKKXNSFWIGLRYTLPLDMNMKMWINGSLTNSLVKLTITDPT----ENDSCAALS 193  
 OY 222 DGAVFAENCILAFSTCOCKRTNH 244  
 DB 194 GDKVTFESCSNDNRWICKCKELYH 216

RESULT 4  
 FCER2\_MOUSE STANDARD; PRT: 331 AA.  
 AC P20693; Q61556; Q61557;  
 DT 01-FEB-1991 (Rel. 17, Created)  
 DT 01-FEB-1991 (Rel. 17, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Low affinity immunoglobulin epsilon FC receptor (lymphocyte IGE  
 DE receptor) (Fc-epsilon-RI) (CD23).  
 GN FCER2 OR FCER2A.  
 OS Mus musculus (Mouse).  
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxId=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=90017519; PubMed=2529542;  
 RA Bettler B., Hofstetter H., Rao M., Yokoyama W.M., Kilchherr F.,  
 RA Conrad D.H.;  
 RT "Molecular structure and expression of the murine lymphocyte low-  
 RT affinity receptor for IGE (Fc epsilon RI)".  
 RL Proc. Natl. Acad. Sci. U.S.A. 86:7566-7570(1989).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE=90171598; PubMed=2137845;  
 RA Golnick S.O., Trounstein M.L., Yamashita L.C., Kehry M.R.,  
 RA Moore K.W.;  
 RT "Isolation, characterization, and expression of cDNA clones encoding

RT the mouse Fc receptor for IGE (Fc epsilon RI)1.1".  
 RL J. Immunol. 144:1974-1982(1990).  
 RN [3]  
 RP SEQUENCE FROM N.A. (FORMS B AND C).  
 RC STRAIN=DEA/2;  
 RX MEDLINE=94372613; PubMed=8086828;  
 RA Kondo H., Ichikawa Y., Nakamura K., Tsuchiya S.;  
 RT "Cloning of cDNAs for new subtypes of murine low-affinity Fc receptor  
 RT for IGE (Fc epsilon RI/CD23)".  
 RL Int. Arch. Allergy Immunol. 105:38-48(1994).  
 RN [4]  
 RP 3D-STRUCTURE MODELING OF LECTIN DOMAIN.  
 RX MEDLINE=94191542; PubMed=8142907;  
 RA Padlan E.A., Helm B.A.;  
 RT "Modeling of the lectin-homology domains of the human and murine low-  
 RT affinity Fc epsilon receptor (Fc epsilon RI/CD23)".  
 RL Receptor 3:325-341(1993).  
 CC -I- FUNCTION: THIS RECEPTOR HAS ESSENTIAL ROLES IN THE REGULATION  
 CC OF IGE PRODUCTION AND IN THE DIFFERENTIATION OF B-CELLS (IT IS  
 CC A B-CELL-SPECIFIC ANTIGEN).  
 CC -I- SUBCELLULAR LOCATION: type II membrane protein.  
 CC -I- ALTERNATIVE PRODUCTS: 3 ISOFORMS; A (SHOWN HERE), B AND C; ARE  
 CC PRODUCED BY ALTERNATIVE SPLICING.  
 CC -I- PTM: N- AND O-GLYCOSYLATED (BY SIMILARITY).  
 CC -I- MISCELLANEOUS: THERE ARE TWO KINDS OF FC RECEPTORS FOR IGE, WHICH  
 CC DIFFER IN BOTH STRUCTURE AND FUNCTION: HIGH AFFINITY RECEPTORS ON  
 CC BASOPHILS AND MAST CELLS AND LOW AFFINITY RECEPTORS ON LYMPHOCYTES  
 CC AND MONOCYTES.  
 CC -I- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.  
 CC -----  
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CC -----

DR EMBL; M99371; AAA74898.1; -;  
 DR EMBL; M34163; AAA37603.1; -;  
 DR EMBL; X64223; CAA45532.1; -;  
 DR EMBL; X64224; CAA45533.1; -;  
 DR PIR; A43518; A43518.  
 DR PDB; 1HLJ; 31-JAN-94.  
 DR MGI; MGI:95497; Fcer2a.  
 DR InterPro: IPR001304; lectin\_c.  
 DR Pfam; PF00059; lectin\_c.1.  
 DR SMART; SM00034; CLECT; 1.  
 DR PROSITE; PS00615; C-TYPE\_LLECTIN.1; 1.  
 DR PROSITE; PS50041; C-TYPE\_LLECTIN.2; 1.  
 KW IGE-binding protein; Transmembrane; Glycoprotein; Receptor; B-cell;  
 KW Repeat; Lectin; Signal-anchor; Alternative splicing; 3d-structure.  
 FT DOMAIN 1 23 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 24 49 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)  
 FT (POTENTIAL).  
 FT DOMAIN 50 331 EXTRACELLULAR (POTENTIAL).  
 FT DOMAIN 185 298 C-TYPE LECTIN (LONG FORM).  
 FT REPEAT 71 91  
 FT REPEAT 92 112  
 FT REPEAT 113 133  
 FT DISULFID 183 311  
 FT DISULFID 186 197  
 FT DISULFID 214 305  
 FT DISULFID 282 296  
 FT CARBOHYD 65 65  
 FT CARBOHYD 114 114  
 FT VARSPLIC 1 7  
 FT VARSPLIC 7 7  
 SQ SEQUENCE 331 AA; 37647 MM; B8C6D5F34ACDDB2 CRC64;

Query Match 14.1%; Score 186; DB 1; Length 331;  
 Best Local Similarity 25.4%; Pred. No. 1.5e-05;

Matches 59; Conservative 43; Mismatches 84; Indels 46; Gaps 9;

QY 25 EESQRELKGIIDITRKLEDEKSEOE-----LLOMIONLOALORANSSEOSREL 77  
 Db 77 OSNOLAKOSQVQMSQNLQLOLAQKQKMAQDSRLSQNLGLQBDLJFNAQSONSKSLQNL 136  
 QY 78 KGRIDTL-----TLKLNKSEQEBELLOKNONLOALOR-----AANSFGCPPOD 122  
 Db 137 NRLODDLVNIRKISGLNKRFPASDSL-----EKLOEVAKLWIEILISKGTACNI---CPKN 189  
 QY 123 WLMHKENCYLF-HGPFGEKRNROTCSLGGOLLOINGADLTFLLQIASTHTSPWIGLH 181  
 Db 190 WLMFQOCYIFGKSKQKQIAFACSDQGLVSHSQKQDPLMQHITNKDS--WIGLO 247  
 QY 182 RKRPGQWLMENGTPLENFQFKTRGVSLQLYSSNCAYLDGAVFANCLII 233  
 Db 248 DLNMEGFVMSDQSPVG-----YSNMNPEPNNGQ-GPDCVWM 285

RESULT 5  
 NK13\_RAT STANDARD; PRT; 223 AA.

DT 01-AUG-1992 (Rel. 23, Created)  
 DT 01-AUG-1992 (Rel. 23, Last sequence update)  
 DT 01-JUN-1994 (Rel. 29, Last annotation update)  
 DE Natural killer cell surface protein p1-3.2.3 (NKR-P1 3.2.3) (Antigen 3.2.3).  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=90378305; PubMed=2399464;  
 RA Giorda R., Rudert W.A., Vavassori C., Chambers W.H.,  
 RA Hiseordt J.C., Trucco W.,  
 RT "NKR-P1, a signal transduction molecule on natural killer cells."; Science 249:1298-1300(1990).  
 RL -1- FUNCTION: MEDIATES TRANSMEMBRANE SIGNALING IN NATURAL KILLER (NK) CELLS AND SO MAY ACT AS A RECEPTOR ABLE TO SELECTIVELY TRIGGER NK CELL ACTIVITY.  
 CC -1- SUBUNIT: HOMODIMER.  
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein.  
 CC -1- TISSUE SPECIFICITY: NATURAL KILLER CELLS.  
 CC -1- MISCELLANEOUS: LIGAND BINDING MAY BE CALCIUM DEPENDENT.  
 CC -1- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.  
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 CC -----  
 CC EMBL: M62891; AAA41710.1; -  
 DR PIR: A35917; A35917.  
 DR InterPro: IPR001304; lectin\_c.  
 DR Pfam: PF00059; lectin\_c.1.  
 DR SMART: SM00034; CLECT.1.  
 DR PROSITE: PS00615; C-TYPE\_LLECTIN\_1; FALSE\_NEG.  
 DR PROSITE: PS50041; C-TYPE\_LLECTIN\_2; 1.  
 KW Glycoprotein; Antigen; Transmembrane; Signal-anchor; Lectin.  
 FT DOMAIN 1 43 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 44 63 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN) (POTENTIAL).  
 FT DOMAIN 64 223 EXTRACELLULAR (POTENTIAL).  
 FT DOMAIN 93 212 C-TYPE LECTIN (LONG FORM).  
 FT DISULFID 94 105 BY SIMILARITY.  
 FT DISULFID 122 210 BY SIMILARITY.  
 FT DISULFID 189 202 BY SIMILARITY.  
 FT CARBOHYD 82 82 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 143 143 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 169 169 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 223 AA; 24551 MW; FCD12B212DDF4330 CRC64;

Query Match 13.28; Score 174; DB 1; Length 223;  
 Best Local Similarity 27.38; Pred. No. 6e-05;  
 Matches 38; Conservative 26; Mismatches 69; Indels 6; Gaps 3;

QY 105 LOEALORANPSG-PCPODMLHKENCY-LFHGPFGEKRNROTCSLGGOLLOINGADL 162  
 Db 79 IOENLSTGSPAKLKCRKDMLSHRDCFHSQTSITWKESLADCGGATLLVQDOBEL 138  
 QY 163 TFLQASHTTSPFWIGLHRRKPGQWLMENGTPLENFQFKTRGVSLQLYSSNCAYLDQ 222  
 Db 139 RFLNLTFRISSEFWIGLSTYLDENKMWINGSTLNSDVLSTGDT-----EKDSCASVSQ 194  
 QY 223 GAVFAENCILAFSICQK 241  
 Db 195 DKVLSESCDSQDNWVCKE 213

RESULT 6  
 CD94\_HUMAN STANDARD; PRT; 179 AA.

ID CD94\_HUMAN  
 AC Q13241;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 15-DEC-1998 (Rel. 37, Last annotation update)  
 DE Natural killer cells antigen CD94 (Kp43) (Killer cell lectin-like receptor subfamily D, member 1).  
 DE receptor subfamily D, member 1).  
 GN KLRD1 OR CD94.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Blood.  
 RX MEDLINE=96011848; PubMed=7589107;  
 RA Chang C., Rodriguez A., Carretero M., Lopez-Botet M., Phillips J.H.,  
 RA Lanier L.L.,  
 RT "Molecular characterization of human CD94: a type II membrane glycoprotein related to the C-type lectin superfamily."; Eur. J. Immunol. 25:2433-2437(1995).  
 RL -1- FUNCTION: PLAYS A ROLE AS A RECEPTOR FOR THE RECOGNITION OF MHC CLASS I HLA-E MOLECULES BY NK CELLS AND SOME CYTOTOXIC T-CELLS.  
 CC -1- SUBUNIT: CAN FORM DISULFIDE-BONDED HETERODIMER WITH NKG2 FAMILY MEMBERS.  
 CC -1- SUBCELLULAR LOCATION: Type II membrane protein.  
 CC -1- TISSUE SPECIFICITY: NATURAL KILLER CELLS.  
 CC -1- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.  
 CC -1- DATABASE: NAME-PROV: NOTE-CD guide CD94 entry;  
 CC WWW=<http://www.ncbi.nlm.nih.gov/prov/cd/cd94.htm>.  
 CC -----  
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 CC -----  
 CC EMBL: U30610; AAC50291.1; -  
 DR MIM: 602894; -  
 DR InterPro: IPR001304; lectin\_c.  
 DR Pfam: PF00059; lectin\_c.1.  
 DR SMART: SM00034; CLECT.1.  
 DR PROSITE: PS00615; C-TYPE\_LLECTIN\_1; FALSE\_NEG.  
 DR PROSITE: PS50041; C-TYPE\_LLECTIN\_2; 1.  
 KW Antigen; Receptor; Glycoprotein; Transmembrane; Signal-anchor; Lectin.  
 FT DOMAIN 1 10 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 11 31 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)

FT	DOMAIN	32	179	(POTENTIAL).	EXTRACELLULAR.	(POTENTIAL).
FT	DOMAIN	98	176	C-TYPE LECTIN (LONG FORM).		
FT	DISULFID	61	72	BY SIMILARITY.		
FT	DISULFID	89	174	BY SIMILARITY.		
FT	DISULFID	152	166	BY SIMILARITY.		
FT	CARBOHYD	83	83	N-LINKED (GLCNAC. . .)	(POTENTIAL).	
FT	CARBOHYD	132	132	N-LINKED (GLCNAC. . .)	(POTENTIAL).	
SO	SEQUENCE	179 AA;	20497 MW;	1884D99EBD9583A7	CRC64;	
Qy	Query Match	12.6%;	Score 166;	DB 1;	Length 179;	
Db	Best Local Similarity	31.6%;	Pred. No. 0.00016;			
Matches	36;	Conservative 20;	Mismatches 48;	Indels 10;	Gaps 4;	
Qy	119 CPDMLMKKNCYLFHG-PFGEMKRRQTCQSLGGGLDQINGDDLFILQAIHSHTSPW	177				
Db	61 COEKWVGRCNCYLFSSBQKTWNSRHLCASQSSLDQNTDELDF--WSSSQQFYW	116				
Qy	178 IGLHRKKKGQOWPLWNGTGPLNFQPFKTRGVSLOLTSSSNC-AYLQDGAFAENC	230				
Db	117 IGLSSEHTTAMLMWNGSALSQYLFP---SEFTNTKNCIAYNNNGNADDESC	166				
RESULT	7					
FCE2-HUMAN	STANDARD;	PRT;	321 AA.			
AC	P06734:					
DT	01-JAN-1988 (Rel. 06, Created)					
DT	01-JAN-1988 (Rel. 06, Last sequence update)					
DT	16-OCT-2001 (Rel. 40, Last annotation update)					
DE	Low affinity immunoglobulin epsilon FC receptor (Lymphocyte Ige					
DE	receptor) (Fc-epsilon-RI) (CD23) (BLAST-2) (Immunoglobulin E-binding					
DE	factor).					
GN	FCER2 OR IGEBP.					
OS	Homo sapiens (Human).					
OC	Eumetazoa; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.					
OX	NCBI_TaxID=9606;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
RX	MEDLINE=87118255; Pubmed=2949326;					
RA	Ikuta K., Takami M., Kim C.W., Honjo T., Miyoshi T., Tagaya Y.,					
RA	Kawabe T., Todoi J.;					
RT	"Human lymphocyte Fc receptor for Ige: sequence homology of its					
RT	cloned cDNA with animal lectins.";					
RL	Proc. Natl. Acad. Sci. U.S.A. 84:819-823(1987).					
RN	[2]					
RP	SEQUENCE FROM N.A.					
RX	MEDLINE=87051737; Pubmed=2877743;					
RA	Kikuchi H., Inui S., Sato R., Barsumian E.L., Owaki H.,					
RA	Yamasaki K., Kaisho T., Uchibayashi N., Hardy R.R., Hirano T.,					
RA	Tsunasawa S., Sakiyama F., Suenura M., Kishimoto T.;					
RT	"Molecular structure of human lymphocyte receptor for immunoglobulin					
RT	E.";					
RL	Cell 47:657-665(1986).					
RN	[3]					
RP	SEQUENCE FROM N.A.					
RX	MEDLINE=87218454; Pubmed=3034567;					
RA	Insulin C., Horstetter H., Sarfelt M., Levy C.A., Suter U., Alaimo D.,					
RA	Klicchener E., Frost H., Desleppse G.;					
RT	"Cloning and expression of the cDNA coding for a human lymphocyte Ige					
RT	receptor.";					
RL	Embo J. 6:109-114(1987).					
RN	[4]					
RP	PARTIAL SEQUENCE, AND DISULFIDE BONDS.					
RX	MEDLINE=93038513; Pubmed=1417742;					
RA	Rose K., Turcatt G., Graber P., Pochon S., Regamey P.-O.,					
RA	Jansen K.U., Magnenet E., Auboney N., Bonney J.-Y.;					
RT	"Partial characterization of natural and recombinant human soluble					
RT	CD23.";					
RL	Biochem. J. 286:819-824(1992).					
RN	[5]					

	R	P	ALTERNATIVE SPLICING.
RX	MEDLINE=69028672; Pubmed-2972386;		
RA	Yokota A., Kikuchi H., Tanaka T., Sato R., Barsamian E.L.,		
RT	Suemura M., Nishimoto T.,		
RT	"Two species of human Fc epsilon receptor II (Fc epsilon RIICD23):		
RL	tissue-specific and IL-4-specific regulation of gene expression.";		
LN	Cell 55:611-618(1988).		
RN	[6]		
RP	3D-STRUCTURE MODELING OF LECTIN DOMAIN.		
RK	MEDLINE=94191542; PubMed-8142907;		
RA	Padlan E.A., Helm B.A.;		
RT	"Modeling of the lectin-homology domains of the human and murine low-		
RL	affinity Fc epsilon receptor (Fc epsilon RIICD23).";		
RN	Receptor 3:325-341(1993).		
RP	[7]		
RK	3D-STRUCTURE MODELING OF ITC-285.		
RA	MEDLINE=96276216; PubMed-8745401;		
RT	Bajorath J., Aruffo A.;		
RL	"Structure-based modeling of the ligand binding domain of the human		
RT	cell surface receptor CD23 and comparison of two independently		
RL	derived molecular models.";		
CC	Protein Sci. 5:240-247(1996).		
CC	-I- FUNCTION: THIS RECEPTOR HAS ESSENTIAL ROLES IN THE REGULATION		
CC	OF ICE PRODUCTION AND IN THE DIFFERENTIATION OF B-CELLS (IT IS		
CC	A B-CELL-SPECIFIC ANTIGEN).		
CC	-I- SUBCELLULAR LOCATION: TYPE II MEMBRANE PROTEIN. ALSO EXISTS AS		
CC	A SOLUBLE EXCRETED FORM.		
CC	-I- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A (SHOWN HERE) AND B; ARE		
CC	PRODUCED BY ALTERNATIVE SPLICING.		
CC	-I- PTM: N- AND O-GLYCOSYLATED.		
CC	-I- MISCELLANEOUS: THERE ARE TWO KINDS OF FC RECEPTORS FOR ICE, WHICH		
CC	DIEFER IN BOTH STRUCTURE AND FUNCTION: HIGH AFFINITY RECEPTORS ON		
CC	BASOPHILS AND MAST CELLS AND LOW AFFINITY RECEPTORS ON LYMPHOCTES		
CC	AND MONOCYTES.		
CC	-I- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.		
CC	-I- DATABASE: NAME=PROW, NOTE=C-D GUIDE CD23 ENTRY:		
CC	WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd23.htm".		
CC	--		
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CC	C ENTITIES REQUIRES A LICENSE AGREEMENT (SEE HTTP://WWW.ISB.SIB.CH/ANNOUNCE/		
CC	C OR SEND AN EMAIL TO LICENSE@ISB.SIB.CH).		
CC	-----		
DR	EMBL; M15059; AAA52434.1; ;		
DR	EMBL; M14766; AAA52435.1; ;		
DR	EMBL; X04772; CAZ8465.1; ;		
DR	EMBL; M23562; AAA52433.1; ;		
DR	PIR; A26067; LNHDUR.		
DR	PIR; A26164; A26164.		
DR	PIR; A26589; A26589.		
DR	PIR; A31924; A31924.		
DR	PIR; JL0132; JL0132.		
DR	PDB; 1HLI; 3J-JAN-94.		
DR	PDB; IKJE; 03-APR-96.		
DR	MIM; 151445; .		
DR	InterPro; IPRO01304; lectin_c.		
DR	pFAM; PF00059; lectin_c_1.		
DR	SMART; SMART0034; CLECT; 1.		
DR	PROSITE; PS00615; C_Type_Lectin_1; 1.		
DR	PROSITE; PS00615; C_Type_Lectin_2; 1.		
KW	IgE-binding protein; Transmembrane; Glycoprotein; Receptor; B-cell;		
KW	Repeat; Lectin; Signal-anchor; Alternative splicing; 3D-structure.		
FT	CHAIN	1	321
FT	DOMAIN	1	150
FT	TRANSMEM	22	47
FT	DOMAIN	48	321
FT	DOMAIN	162	284
FT	SITE	149	150

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FT REPEAT 69 89
FT REPEAT 90 110
FT REPEAT 111 131
FT DISULFID 160 288 BY SIMILARITY.
FT DISULFID 163 174 BY SIMILARITY.
FT DISULFID 191 282
FT DISULFID 255 273
FT CARBOHYD 63 63
FT CARBOHYD 269 269 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CONFLICT 269 269 MEGQYS -> NMPQSO (IN ISOFORM B).
FT CONFLICT 269 269 N -> T (IN REF. 3).
SQ SEQUENCE 321 AA; 36468 MW; F86708C0E6515887 CRC64;

Query Match 12.5%; Score 165.5; DB 1; Length 321;
Best Local Similarity 28.7%; Pred. No. 0.00032;
Matches 51; Conservative 33; Mismatches 75; Indels 19; Gaps 7;

QY 28 QRELKGRIDITRKDEKSEKEEL---LQMKONLQEAQORANSESEQRELKGRIDT 83
DB 78 QMAKQSTQISQLEELRAEQRLKSQDLELWNL-NGIQ-ADLSSFKSQELNER-- 131
QY 84 LTLKNEKSEKEELQKONLQEAQORANF-SGPCPQDMLMKKCYLF-HGPFQMEK 141
DB 132 -----NEASDLERLREYVKRLMELQVSSGFCNCTPEKMINFQKCYFEGKGTQWVH 186
QY 142 NRQTCQSLGGQLQINGADDLTFLQAIISHTSPFWIGLHRRKPGQPMLENGTPINF 199
DB 187 ARYACDMEQGLVSIHSPEDQFLTKHSHSGS--WIGLNLDLKGFIEWDGSVDY 242

RESULT 8
LECT_HUMAN STANDARD; PRT; 311 AA.
ID LECT_HUMAN STANDARD; PRT; 311 AA.
AC P07307;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Asialoglycoprotein receptor 2 (Hepatic lectin H2) (ASGP-R) (ASGPR).
GN ASGR2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86016723; PubMed=3863106;
RA Spiess M., Lodish H.F.;
RT "Sequence of a second human asialoglycoprotein receptor: conservation
RT of two receptor genes during evolution."
RL Proc. Natl. Acad. Sci. U.S.A. 82:6465-6469(1985).
CC -1- FUNCTION: MEDIATES THE ENDOCYTOSIS OF PLASMA GLYCOPROTEINS TO
CC WHICH THE TERMINAL SIALIC ACID RESIDUE ON THEIR COMPLEX
CC CARBOHYDRATE MOIETIES HAS BEEN RESIDUE. THE RECEPTOR RECOGNIZES
CC TERMINAL GALACTOSE AND N-ACETYLGLUCOSAMINE UNITS. AFTER LIGAND
CC BINDING TO THE RECEPTOR, THE RESULTING COMPLEX IS INTERNALIZED AND
CC TRANSPORTED TO A SORTING ORGANELLE, WHERE RECEPTOR AND LIGAND ARE
CC DISSOCIATED. THE RECEPTOR THEN RETURNS TO THE CELL MEMBRANE
CC SURFACE.
CC -1- SUBUNIT: THE FUNCTIONING LIGAND-BINDING UNIT OF THIS RECEPTOR
CC IS THOUGHT TO BE AT LEAST A DIMER.
CC -1- SUBCELLULAR LOCATION: Type II membrane protein.
CC -1- TISSUE SPECIFICITY: EXPRESSED EXCLUSIVELY IN HEPATIC PARENCHYMAL
CC CELLS.
CC -1- MISCELLANEOUS: CALCIUM IS REQUIRED FOR LIGAND BINDING.
CC -1- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC or send an email to license@isb-sib.ch).

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CC -----
CC EMBL: M11025; AAB59519.1; -.
CC PIR: A25179; LNHU2A.
CC HSSP: P06734; IKJE.
CC MIM: 108361; -.
CC InterPro: IPR001304; lectin_C.
CC Pfam: PF00059; lectin_c; 1.
CC SMART: SM00034; CLECT; 1.
CC PROSITE: PS00615; C-TYPE_LECTIN_1; 1.
CC PROSITE: PS50041; C-TYPE_LECTIN_2; 1.
CC Lectin: Glycoprotein; Receptor; Endocytosis; Transmembrane;
CC Calcium; Signal-anchor; Phosphorylation.
CC DOMAIN 1 58 CYTOPLASMIC (POTENTIAL).
CC TRANSMEM 59 79 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
CC FT DOMAIN 80 311 (POTENTIAL).
CC FT SITE 176 302 EXTRACELLULAR (POTENTIAL).
CC FT SITE 5 8 C-TYPE LECTIN (LONG FORM).
CC FT DISULFID 177 188 BY SIMILARITY.
CC FT DISULFID 205 300 BY SIMILARITY.
CC FT DISULFID 278 292 BY SIMILARITY.
CC FT CARBOHYD 102 102 N-LINKED (GLCNAC. .).
CC FT CARBOHYD 170 170 N-LINKED (GLCNAC. .).
CC FT CARBOHYD 305 305 N-LINKED (GLCNAC. .).
CC MOD_RES 12 12 PHOSPHORYLATION.
SQ SEQUENCE 311 AA; 35191 MW; 82C78FEC8FBA316 CRC64;

Query Match 12.5%; Score 164.5; DB 1; Length 311;
Best Local Similarity 25.1%; Pred. No. 0.00036;
Matches 59; Conservative 36; Mismatches 81; Indels 59; Gaps 11;

QY 51 ELQMKONLQEAQORANSS-----ESSQRELKGRIDT 85
DB 88 QLQELSLKLEAFNFSSTLEVOAISTHGSVGDKITSLGAKLEKQODLKHADL 147
QY 86 LKLNKESKE-----QELLQKONLQEAQORANFSGPCPQDMLMKKCYLF-HGPFQ 138
DB 148 FHLKHFVDLRFVACQMLHLSNGS-----QRTC-----CPVNVVEHQSGCYWFSHGKA 197
QY 139 WEKNRQTCQSLGGQLQINGADDLTFLQAIISHTSPF--WIGLHRRKPGQPMLENGTPI 196
DB 198 WAEAEKTCOLENAHLVYINSHEQKFTVQ-----HTNFPNWIGL--TDSGSKWNVGCTD 251
QY 197 LNFQFETRGVSL-----QLYSSSNCAVYL-DGAVFAENCILIAFSICQKTN 243
DB 252 YRHN-YKNMVAVTQDNHGHGELGSEDCVEYQPDGRWNNDPCLQVYRWVCCKRRN 305

RESULT 9
KUCR_RAT STANDARD; PRT; 550 AA.
ID KUCR_RAT STANDARD; PRT; 550 AA.
AC P10716;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Kupfer cell receptor.
GN KCLR.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxId=10116;
RN [1]
RP SEQUENCE FROM N.A. AND SEQUENCE OF 83-104.
RX MEDLINE=88227939; PubMed=2836387;
RA Hoyle G.W., Hill R.L.;
RT "Molecular cloning and sequencing of a cDNA for a carbohydrate
RT binding receptor unique to rat Kupfer cells."
RL J. Biol. Chem. 263:7487-7492(1988).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=91107689; PubMed=1846367;
RA Hoyle G.W., Hill R.L.;

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ID	NAME	STANDARD	PRT	231 AA
AC	26717; 043802;			
DT	01-AUG-1992 (Rel. 23, Created)			
DT	01-MAR-2002 (Rel. 41, Last sequence update)			
DT	01-MAR-2002 (Rel. 41, Last annotation update)			
DE	<p>           NKG2-C type II integral membrane protein (NKG2-C activating NK receptor).            GN KLRG2 OR NKG2C.            OS Homo sapiens (Human).            OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.            OX NCBI_TaxID=9606;            RN [1].            RP SEQUENCE FROM N.A.            RX MEDLINE=91178434; PubMed=2007850;            RA Houchins J.P., Yabe T., McSherry C., Bach F.H.;            RT "DNA sequence analysis of NKG2, a family of related cDNA clones encoding type II integral membrane proteins on human natural killer cells.";            RT J. Exp. Med. 173:1017-1020(1991).            RN [2].            RP SEQUENCE FROM N.A.            RX MEDLINE=96350122; PubMed=9683661.            RA Glienne J., Sobhanov Y., Brostjan C., Steffens C., Nguyen C., Lehrach H., Hofer E., Francis F.;            RT "The genomic organization of NKG2C, E, F, and D receptor genes in the human natural killer gene complex.";            RN Immunogenetics 48:163-173(1998).            RN [3].            RP SEQUENCE FROM N.A.            RC TISSUE=Lymphoid;            RA Blasson R.;            RL Submitted (MAY-1997) to the EMBL/GenBank/DDBJ databases.            CC -!- FUNCTION: PLAYS A ROLE AS A RECEPTOR FOR THE RECOGNITION OF MHC CLASS I HLA-E MOLECULES BY NK CELLS AND SOME CYTOTOXIC T-CELLS.            CC -!- SUBUNIT: CAN FORM DISULFIDE-BONDED HETERODIMER WITH CD94.            CC -!- SUBCELLULAR LOCATION: Type II membrane protein.            CC -!- TISSUE SPECIFICITY: NATURAL KILLER CELLS.            CC -!- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.         </p>			
CC	<p>           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <a href="http://www.isb-sib.ch/announce/or_send_an_email_to_license@isb-sib.ch">http://www.isb-sib.ch/announce/or_send_an_email_to_license@isb-sib.ch</a>).            -----         </p>			
CC	EMBL; X54869; CAA3651.1; -			
DR	EMBL; AJ001684; CAA04922.1; -			
DR	EMBL; Y13055; CAA73498.1; -			
DR	PIR; P0374; P0374.			
DR	MTM; 602891; -			
DR	InterPro; IPR001304; lectin.c.			
DR	Pfam; PF00059; lectin.c; 1.			
DR	SMART; SM00034; CLECT.1.			
DR	PROSITE; PS00615; C-TYPE_LECTIN_1; FALSE_NEG.			
DR	PROSITE; PS00041; C-TYPE_LECTIN_2; 1.			
KW	Receptor; Transmembrane; Multigene family; Signal-anchor; Lectin; Glycoprotein.			
FT	DOMAIN	1	70	CYTOPLASMIC (POTENTIAL).
FT	TRANSSEM	71	93	SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN) (POTENTIAL).
FT	DOMAIN	94	231	EXTRACELLULAR (POTENTIAL).
FT	DISULEID	116	229	C-TYPE LECTIN (LONG FORM).
FT	DISULEID	117	128	BY SIMILARITY.
FT	DISULEID	145	227	BY SIMILARITY.
FT	DISULEID	206	219	BY SIMILARITY.
FT	CARBOHYD	100	100	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	149	149	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	178	178	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CONFLICT	161	161	M -> I (IN REF. 1).

SQ SEQUENCE 231 AA; 26072 MW; 6B971EECD7542930 CRC64;  
 Query Match 12.3%; Score 162.5; DB 1; Length 211;  
 Best Local Similarity 23.0%; Pred. No 0.00035;  
 Matches 53; Conservative 37; Mismatches 101; Indels 39; Gaps 7;  
 QY 18 SCGRKPKESQRELKGIKIDITRKLDKSKQEBELLQMIQLOA-----LQR 65  
 Db 12 SLADDPKRO-QRKPKKSSSI-----SGTEGEIFQVELNLQNPISLHOCIDKIDYDQG 63  
 QY 66 AANSSESOBELKGIKIDITRKLDKSKQEBELLQMIQLOAORANSGPQPMW 125  
 Db 64 LRPPELVAEVLGILICIVLMAVTLKIVLIPLEQNNSSPNTQKARRCGHCPERMIT 123  
 QY 126 HKENCYLFHGPFG-----MEKNROTQSLGGLQINGADLPITLQASHITSPFWIG 180  
 Db 124 YNSCYT-----IGKERTWESLACTSKNSSLSTINEEMKFLASILPSS-----WIGV 175  
 QY 181 HRRKPGQPMLENGTPLNFQFETRGVSLQLYSSNCAYLQDGAFAENC 230  
 b 176 FRSSHHPTVITINGLAFKHKIKSDNAEL-----NCAYLVNRLKSAOC 219  
 RESULT 11  
 KUCR\_MOUSE STANDARD; PRT; 548 AA.  
 AC F70194;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 16-OCT-2001 (Rel. 40, Last annotation update)  
 DE Kupfer cell receptor.  
 GN KCLR.  
 OS Mus musculus (mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BALB/C; TISSUE-Liver;  
 RA Takekawa R., Nagatsuma H., Nomoto C., Watanabe Y., Akaike T.;  
 RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.  
 CC - FUNCTION: RECEPTOR WITH AN AFFINITY FOR GALACTOSE AND FUCOSE.  
 CC - COULD BE INVOLVED IN ENDOCYTOSIS.  
 CC - SUBCELLULAR LOCATION: TYPE II membrane protein.  
 CC - TISSUE SPECIFICITY: KUPFER CELLS.  
 CC - SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.  
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 CC  
 CC EMBL; D88577; BAA13647.1; -  
 DR HSSP; P20693; IHLI.  
 DR MGD; MGI:1859834; Kclr.  
 DR InterPro: IPR001304; Lectin\_c.  
 DR Pfam: PF00059; Lectin\_c; 1.  
 DR SMART; SM00034; CLECT; 1.  
 DR PROSITE; PS00615; C-TYPE\_LECTIN\_1; 1.  
 DR PROSITE; PS50041; C-TYPE\_LECTIN\_2; 1.  
 KM Receptor; Transmembrane; Glycoprotein; Lectin; Signal-anchor;  
 Endocytosis.  
 FT DOMAIN 1 42 CYTOPLASMIC (POTENTIAL).  
 FT TRANSMEM 43 69 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)  
 FT DOMAIN 70 548 EXTRACELLULAR (POTENTIAL).  
 FT DISULFID 438 538 C-TYPE LECTIN (SHORT FORM).  
 FT DISULFID 440 536 BY SIMILARITY.  
 FT DISULFID 516 528 BY SIMILARITY.

FT CARBOHYD 86 86 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 92 92 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 115 115 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 132 132 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 209 209 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 255 255 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 548 AA; 61268 MW; 6F6495E820E73BD9 CRC64;  
 Query Match 12.2%; Score 160.5; DB 1; Length 548;  
 Best Local Similarity 25.5%; Pred. No 0.0012;  
 Matches 56; Conservative 36; Mismatches 93; Indels 35; Gaps 9;  
 QY 2 TFDKMKRPN---DEPDQSCGRKPKESQRELKGIKIDITRKLDKSKQEBELLQMIQLOA 54  
 Db 283 TLTAQTQKANGHLQPTDAIQGLKAEIKSTSLNSRIEYVNGQKDAARELQTLRLDLS 342  
 QY 55 -----MIQNLQELQRAANSSESOBELKGIKIDITRKLDKSKQEBELLQMIQLOA 99  
 Db 343 VSALKSNVOMIQSLQRAKTEMQTLKADLA-TRALAKIQGEONRLGALQEAAYAAQOE 401  
 QY 100 QKNQNLQELQRAANSSESOBELKGIKIDITRKLDKSKQEBELLQMIQLOA 158  
 Db 402 QKTQN--QVLDLA-----QNMKRYNGNFTYRSBKPKRREKCTSGAHLASVTS 452  
 QY 159 ADLFTFLQALISHTSPFWIGLARRKPGQPMLENGTPLN 198  
 Db 453 QEQAFVLYQTTSS--SGDHWIGLTDQGTGEGIRWVWDGTPFN 490  
 RESULT 12  
 NKGE\_HUMAN STANDARD; PRT; 240 AA.  
 AC 007444;  
 DT 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 01-MAR-2002 (Rel. 41, Last annotation update)  
 DE NKG2-E type II integral membrane protein (NKG2-D activating NK  
 receptor).  
 GN KLRC3 OR NKG2E.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=94102823; PubMed=8276468;  
 RA Aamkiewicz T.V., McSherry C., Bach F.H., Houchins J.P.;  
 RT "Natural killer lectin-like receptors have divergent carboxy-terminal,  
 distinct from C-type lectins.";  
 RL Immunogenetics 39:218-218(1994).  
 CC - FUNCTION: PLAYS A ROLE AS A RECEPTOR FOR THE RECOGNITION OF MHC  
 CLASS I HLA-E MOLECULES BY NK CELLS AND SOME CYTOTOXIC T-CELLS.  
 CC - SUBUNIT: CAN FORM DISULFIDE-BONDED HETERODIMER WITH CD94.  
 CC - TISSUE SPECIFICITY: NATURAL KILLER CELLS.  
 CC - SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC MEDLINE=98350122; PubMed=9683661;  
 RA Glenske J., Sobanov Y., Brostjan C., Steffens C., Nguyen C.,  
 RA Lehmich H., Hoter E., Francis F.;  
 RT "The genomic organization of NKG2C, E, F, and D receptor genes in the  
 human natural killer gene complex.";  
 RL Immunogenetics 48:163-173(1998).  
 CC - FUNCTION: PLAYS A ROLE AS A RECEPTOR FOR THE RECOGNITION OF MHC  
 CLASS I HLA-E MOLECULES BY NK CELLS AND SOME CYTOTOXIC T-CELLS.  
 CC - SUBUNIT: CAN FORM DISULFIDE-BONDED HETERODIMER WITH CD94.  
 CC - TISSUE SPECIFICITY: NATURAL KILLER CELLS.  
 CC - SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC

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CC -----
DR EMBL; L14542; AAA16833.1;
DR EMBL; AJ001685; CAA04923.1;
DR MIM; 602892;
DR InterPro; IPR001304; lectin_c.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C-TYPE LECTIN_1; FALSE_NEG.
DR PROSITE; PS50041; C-TYPE LECTIN_2; 1.
KW Receptor; Transmembrane; Multigene family; Signal-anchor; Lectin;
KW Glycoprotein.
FT DOMAIN 1 70 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 71 93 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT DOMAIN 94 240 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 116 230 C-TYPE LECTIN (LONG FORM).
FT DISULFID 117 128 BY SIMILARITY.
FT DISULFID 207 220 BY SIMILARITY.
FT CARBOHYD 100 100 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 149 149 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 179 179 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 240 AA; 27012 MW; 20691FB2127AD8A6 CRC64;

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Query Match 12.1%; Score 159; DB 1; Length 240;
Best Local Similarity 22.9%; Pred. No. 0.00061;
Matches 53; Conservative 40; Mismatches 98; Indels 40; Gaps 8;

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QY 18 SCGKKPKESQRELKGIIDITRKLEKSEDELLQMIQIOEA-----LQR 65
DB 12 SLADDPKPO-QRKPKGNSSSI-----SGTEQEIFQVELNQNLSLHNOGIDKIDYDCG 63
QY 66 AANSEESQRELKGIIDITRKLEKSEDELLQMIQIOEA-----LQR 125
DB 64 LLPEPKLTAELVGLITCYLMATVLTIVLPPELQNNSSPRTKQKAPCHCEBEMIT 123
QY 126 HKENCYLFEHGPFG-----WEKNRQTCQSL-GGQLQINGADDLPFLQAISSHTSPFWIG 179
DB 124 YSNQCY----IGKERRTWESLQACASKNSSLSIDNEEMKFLASILPSS-----WIG 175
QY 180 LHRKKPGQPMWENGTPLPFOFRTKRGVSLQYSSNCAYLQDGAFAENC 230
DB 176 VFRNSHHWPVTINGLAFKHE-----IKSDHARNCAMLHVRLISDOC 220

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RESULT 13
ID NKGD_HUMAN STANDARD; PRT; 216 AA.
AC P26718;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE NKG2-D type II integral membrane protein (NKG2-D activating NK
DE receptor).
GN KLRK4 OR NKG2D.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91178434; PubMed=2007850;
RA Houchns J.P., Yabe T., McSherry C., Bach F.H.;
RT "DNA sequence analysis of NKG2, a family of related cDNA clones
RT encoding type II integral membrane proteins on human natural killer
RT cells.";
RL J. Exp. Med. 173:1017-1020(1991).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=98350122; PubMed=9683661;
RA Gijente J., Sobanov Y., Brostjan C., Steffens C., Nguyen C.,
RA Leinrich H., Hoter E., Francis F.;
RT "The genomic organization of NKG2C, E, F, and D receptor genes in the

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RT human natural killer gene complex.";
RL Immunogenetics 48:163-173(1998).
CC -!- FUNCTION: PLAYS A ROLE AS A RECEPTOR FOR THE RECOGNITION OF MHC
CC CLASS I HLA-E MOLECULES BY NK CELLS AND SOME CYTOTOXIC T-CELLS.
CC -!- SUBUNIT: CAN FORM DISULFIDE-BONDED HETERODIMER WITH CD94.
CC -!- SUBCELLULAR LOCATION: Type II membrane protein.
CC -!- TISSUE SPECIFICITY: NATURAL KILLER CELLS.
CC -!- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
CC -----
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DR EMBL; X54870; CAA38652.1;
DR EMBL; AJ001687; CAA04925.1;
DR EMBL; AJ001688; CAA04925.1; JOINED.
DR EMBL; AJ001689; CAA04925.1; JOINED.
DR PIR; P03375; P03375.
DR PIR; S19110; S19110.
DR MIM; 602893;
DR InterPro; IPR001304; lectin_c.
DR Pfam; PF00059; lectin_c; 1.
DR SMART; SM00034; CLECT; 1.
DR PROSITE; PS00615; C-TYPE LECTIN_1; FALSE_NEG.
DR PROSITE; PS50041; C-TYPE LECTIN_2; 1.
KW Receptor; Transmembrane; Multigene family; Signal-anchor; Lectin;
KW Glycoprotein.
FT DOMAIN 1 51 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 52 72 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT DOMAIN 73 216 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 98 213 C-TYPE LECTIN (LONG FORM).
FT DISULFID 99 110 BY SIMILARITY.
FT DISULFID 127 211 BY SIMILARITY.
FT DISULFID 189 203 BY SIMILARITY.
FT CARBOHYD 131 131 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 163 163 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 202 202 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 216 AA; 25274 MW; C22F6BD533D7800E CRC64;

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Query Match 12.0%; Score 158.5; DB 1; Length 216;
Best Local Similarity 27.6%; Pred. No. 0.00059;
Matches 40; Conservative 26; Mismatches 62; Indels 17; Gaps 5;

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QY 102 NONLEALORANFSGPCPODMLMKHENCY-LFHGPFGEKRNQTCQSLGGQLQINGAD 160
DB 84 NOEVOIPL--TESYCGPCFKNNICYNKCTOFFDESKNMYESQASCSQNASLKYKSE 141
QY 161 DLFTFLQAISSHTSPFWIGLARRKPGQPMWENGTPLN---PQFRTKRGVSLQYSSNC 217
DB 142 DODLLKLVKSY----HMMGLVHIPTNGSNQWEDGSLISNLITLTIEMQGDCAVASSRK 197
QY 218 ATLQDGAFAVENCILIASICOKKT 242
DB 198 GYI-----ENCSTPNYICMORT 215

```

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RESULT 14
ID KLR5_MOUSE STANDARD; PRT; 266 AA.
AC Q60652;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Killer cell lectin-like receptor 5 (T-cell surface glycoprotein
DE LY-49E) (LY49-E antigen).
GN KLR5 OR LY49E OR LY-49E OR LY49-E.
OS Mus musculus (Mouse).

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OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Spleen;
RX MEDLINE=94300068; PubMed=8027540;
RA Smith H.R.C., Karhofer F.M., Yokoyama W.M.;
RT "Ly-49 multigene family expressed by IL-2-activated NK cells.";
RL J. Immunol. 153:1068-1079(1994).
CC -1- FUNCTION: RECEPTOR ON NATURAL KILLER (NK) CELLS FOR CLASS I MHC.
CC -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED.
CC -1- SUBCELLULAR LOCATION: Type II membrane protein.
CC -1- SIMILARITY: CONTAINS 1 C-TYPE LECTIN FAMILY DOMAIN.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC or send an email to license@isb-sib.ch).
DR EMBL: U10091; AAA50219.1;
DR MGI: 101903; K1ra5.
DR InterPro: IPR001304; Lectin_C.
DR Pfam: PF00059; Lectin_c; 1.
DR SMART: SM00034; CLECT; 1.
DR PROSITE: PS00615; C-TYPE LECTIN_1; FALSE_NEG.
DR PROSITE: PS00041; C-TYPE LECTIN_2; 1.
KW T-cell; Glycoprotein; Antigen; Receptor; Transmembrane; Cell adhesion;
KW Signal-anchor; Lectin; Receptor; Multigene family.
FT DOMAIN 1 44 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 45 66 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT 67 266 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 143 261 C-TYPE LECTIN (LONG FORM).
FT DISULFID 171 257 BY SIMILARITY.
FT 236 249 BY SIMILARITY.
FT CARBOHYD 87 87 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 104 104 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 250 250 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 266 AA; 30843 MW; B8B07F221875049C CRC64;

Query Match 11.8%; Score 156; DB 1; Length 266;
Best Local Similarity 27.6%; Pred. No. 0.0011;
Matches 54; Conservative 30; Mismatches 96; Indels 16; Gaps 8;

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DE Early activation antigen CD69 (Early T-cell activation antigen p60)
DE (GP32/28) (Leu-23) (MUR-3) (EAI) (BL-AC/P26) (Activation Inducer
DE molecule) (AIM).
GN CD69.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=93267093; PubMed=8496594;
RA Hamann J., Flebig H., Strauss M.;
RT "Expression cloning of the early activation antigen CD69, a type II
RT integral membrane protein with a C-type lectin domain.";
RL J. Immunol. 150:4920-4927(1993).
RN [2]
RP SEQUENCE FROM N.A. AND SEQUENCE OF 96-103; 128-146 AND 189-199.
RC TISSUE=Blood;
RX MEDLINE=93340630; PubMed=8340758;
RA Lopez-Cabrera M., Santis A.G., Fernandez-Ruiz E., Blacher R.,
RA Esch F., Sanchez-Mateos P., Sanchez-Madrid F.;
RT "Molecular cloning, expression, and chromosomal localization of the
RT human earliest lymphocyte activation antigen AIM/CD69, a new member
RT of the C-type animal lectin superfamily of signal-transmitting
RT receptors.";
RL J. Exp. Med. 178:537-547(1993).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=93314711; PubMed=8100776;
RA Ziegler S.F., Ramsdell F., Hjerrild K.A., Armitage R.J.,
RA Grabstein K.H., Hennen K.B., Farrah T., Fanslow W.C., Shevach E.M.,
RA Alderson M.R.;
RT "Molecular characterization of the early activation antigen CD69: a
RT type II membrane glycoprotein related to a family of natural killer
RT cell activation antigens.";
RL Eur. J. Immunol. 23:1643-1648(1993).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=94298875; PubMed=8026529;
RA Santis A., Lopez-Cabrera M., Hamann J., Strauss M., Sanchez-Madrid F.;
RT "Structure of the gene coding for the human early lymphocyte
RT activation antigen CD69: a C-type lectin receptor evolutionarily
RT related with the gene families of natural killer cell-specific
RT receptors.";
RL Eur. J. Immunol. 24:1692-1697(1994).
CC -1- FUNCTION: INVOLVED IN LYMPHOCYTE PROLIFERATION AND FUNCTIONS AS A
CC SIGNAL TRANSMITTING RECEPTOR IN LYMPHOCYTES, NATURAL KILLER (NK)
CC CELLS, AND PLATELETS.
CC -1- SUBUNIT: HOMODIMER; DISULFIDE-LINKED.
CC -1- SUBCELLULAR LOCATION: Type II membrane protein.
CC -1- TISSUE SPECIFICITY: EXPRESSED ON THE SURFACE OF ACTIVATED T CELLS,
CC B-CELLS, NATURAL KILLER CELLS, NEUTROPHILS, EOSINOPHILS, EPIDERMAL
CC LANGERHANS CELLS AND PLATELETS.
CC -1- DEVELOPMENTAL STAGE: EARLIEST INDUCIBLE CELL SURFACE GLYCOPROTEIN
CC ACQUIRED DURING LYMPHOID ACTIVATION.
CC -1- INDUCTION: BY ANTIGENS, MITOGENS OR ACTIVATORS OF PKC ON THE
CC SURFACE OF T AND B LYMPHOCYTES. BY INTERACTION OF IL-2 WITH THE
CC P75 IL-2R ON THE SURFACE OF NK CELLS.
CC -1- PTM: CONSTITUTIVE SER/THR PHOSPHORYLATION IN BOTH MATURE
CC THYMOCYTES AND ACTIVATED T LYMPHOCYTES.
CC -1- DATABASE: NAME=PRO; NOTE=CD guide CD69 entry;
CC WWW="http://www.ncbi.nlm.nih.gov/prov/cd/cd69.htm".
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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DR EMBL; L07555; AAB46359.1; -  
DR EMBL; Z22576; CAA80298.1; -  
DR EMBL; Z30426; CAA83017.1; -  
DR EMBL; Z30430; CAA83017.1; JOINED.  
DR EMBL; Z30427; CAA83017.1; JOINED.  
DR EMBL; Z30429; CAA83017.1; JOINED.  
DR EMBL; Z30428; CAA83017.1; JOINED.  
DR PIR; JH0822; JH0822.  
DR MIM; 107273; -  
DR InterPro: IPR001304; lectin\_c.  
DR Pfam; PF00059; lectin\_c; 1.  
DR SMART; SM00034; CLECT; 1.  
DR PROSITE; PS00615; C-TYPE LECTIN\_1; FALSE\_NEG.  
DR PROSITE; PS50041; C-TYPE LECTIN\_2; 1.  
KW Antigen: B-cell; Glycoprotein; Transmembrane; Lectin; Signal-anchor;  
KW Phosphorylation.  
FT DOMAIN 1 40 CYTOPLASMIC (POTENTIAL).  
FT TRANSMEM 41 61 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)  
FT DOMAIN 62 199 (POTENTIAL).  
FT DOMAIN 67 199 EXTRACELLULAR (POTENTIAL).  
FT DISULFID 68 85 C-TYPE LECTIN (LONG FORM).  
FT DISULFID 96 194 BY SIMILARITY.  
FT DISULFID 173 186 BY SIMILARITY.  
FT CARBOHYD 166 166 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 199 AA; 22559 MM; 172E269D2FB8DFB CRC64;

Query Match 11.7%; Score 154.5; DB 1; Length 199;  
Best Local Similarity 27.6%; Pred. No. 0.00097;  
Matches 37; Conservative 18; Mismatches 60; Indels 19; Gaps 6;

OY 115 FSGP-----CPQDWLHKENCYLFHG-PFGMEKNROTCQSLGGQLQINGADDLTFIL 166  
DB 74 FSPEDSHVSSCESEWVGQKRCYFISTYKRSTSAQNAACSEHGATLAVIDSEKDMNPLK 133  
OY 167 QAISHTSPFWIGLHRRKPGQPMWENGTPLNFOFFKTRGVSLQLYSSNCAYLQDGAYF 226  
DB 134 RYAGR--EEHWGL-KKEPGHPKWSNGKEFN-NMENVLTG-----SDKCYELKNTVEYS 182  
OY 227 AENCILIAFSTCOK 240  
DB 183 SMECEKNLYWICK 196

Search completed: August 19, 2002, 23:06:57  
Job time: 528 sec

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GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: August 19, 2002, 22:57:24 ; Search time 68.99 Seconds  
(without alignments)  
619.361 Million cell updates/sec

Title: US-09-898-554-14  
Perfect score: 1319  
Sequence: 1 MTFDDKMKRPANDEPDQKSCG.....ENCILAFSICQKTNHLQI 247

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues  
Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

1: SP archaea:\*  
2: SP bacteria:\*  
3: SP fungi:\*  
4: SP human:\*  
5: SP invertebrate:\*  
6: SP mammal:\*  
7: SP mhc:\*  
8: SP organelle:\*  
9: SP phage:\*  
10: SP plant:\*  
11: SP rodent:\*  
12: SP virus:\*  
13: SP vertebrate:\*  
14: SP unclassified:\*  
15: SP virus:\*  
16: SP bacteriap:\*  
17: SP archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1241	94.1	363	11 09EQ09	09EQ09 mus musculus
2	972	73.7	364	11 070156	070156 ratius norv
3	643	48.4	278	6 09XTA8	09XTA8 oryctolagus
4	639	48.4	274	6 09TTK7	09TTK7 sus scrofa
5	637	48.3	273	4 P78380	P78380 homo sapien
6	596	45.2	270	6 P79391	P79391 bos taurus
7	258	19.6	247	4 09BXN2	09BXN2 homo sapien
8	251.5	19.1	168	4 096PA7	096PA7 homo sapien
9	251	19.0	201	4 09H1K3	09H1K3 homo sapien
10	231	17.5	244	11 09J150	09J150 mus musculus
11	224.5	17.0	381	6 09SLA8	09SLA8 macaca mula
12	223.5	16.9	381	6 09SLC6	09SLC6 macaca neme
13	223	16.9	360	4 096Q04	096Q04 homo sapien
14	223	16.9	380	4 096Q05	096Q05 homo sapien
15	223	16.9	380	4 096Q00	096Q00 homo sapien
16	223	16.9	404	4 09NNX6	09NNX6 homo sapien

17	223	16.9	404	4 096Q01	096Q01 homo sapien
18	222.5	16.9	404	6 095J96	095J96 macaca mula
19	221	16.8	280	4 09NZH3	09NZH3 homo sapien
20	219.5	16.6	223	11 092563	092563 mus musculus
21	218.5	16.6	217	11 064228	064228 mus sp. nki
22	216.5	16.4	275	11 09D403	09D403 mus musculus
23	212	16.1	268	4 096Q03	096Q03 homo sapien
24	212	16.1	404	6 095198	095198 pan troglod
25	211	16.0	334	4 096Q09	096Q09 homo sapien
26	210	15.9	398	4 096Q08	096Q08 homo sapien
27	206.5	15.7	227	11 092564	092564 mus musculus
28	205	15.5	312	4 096Q07	096Q07 homo sapien
29	204.5	15.5	223	11 099JB4	099JB4 mus musculus
30	204.5	15.5	223	11 099P32	099P32 mus musculus
31	203.5	15.4	295	11 0912M4	0912M4 mus musculus
32	203.5	15.4	311	11 09DBV4	09DBV4 mus musculus
33	203.5	15.4	325	11 091X20	091X20 mus musculus
34	202.5	15.4	227	11 061973	061973 mus musculus
35	201.5	15.3	227	11 091V25	091V25 mus musculus
36	200.5	15.2	223	11 092565	092565 mus musculus
37	195.5	14.8	224	11 061970	061970 mus musculus
38	192.5	14.6	189	11 061969	061969 mus musculus
39	192.5	14.6	263	4 096Q03	096Q03 homo sapien
40	191.5	14.5	229	11 09JL99	09JL99 mus musculus
41	191	14.5	332	4 096Q05	096Q05 homo sapien
42	190	14.4	309	11 063097	063097 ratius norv
43	189.5	14.4	198	11 09DBL1	09DBL1 mus musculus
44	187.5	14.2	156	13 073894	073894 gallus gall
45	186.5	14.1	230	11 054871	054871 ratius norv

## ALIGNMENTS

RESULT 1  
ID 09EQ09 PRELIMINARY: PRT; 363 AA.  
AC 09EQ09;  
DT 01-MAR-2001 (TREMBLrel. 16, Created)  
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
DE 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
DE OXIDIZED LDL RECEPTOR.  
OS LOX-1.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Park S.-H., Ahn H.-J., Cho J.-J.;  
RT "Mouse LOX-1 is expressed in mast cells after Ige cross-linking.";  
RL Submitted (SEP-2000) to the EMBL/Genbank/DBO databases.  
DR EMBL; AF305744; AAC44998.1; -;  
DR InterPro; IPR001304; Lectin\_C.  
DR Pfam; PF000059; Lectin\_C; 1.  
DR SMART; SM00034; CLECT; 1.  
DR PROSITE; PS0041; C\_Type\_Lectin\_2; 1.  
KW Receptor.  
SQ SEQUENCE 363 AA; 41613 MW; E44703D6408F15F8 CRC64;

Query Match 94.1%; Score 1241; DB 11; Length 363;  
Best Local Similarity 67.5%; Pred. No. 4,6e+80;  
Matches 245; Conservative 0; Mismatches 2; Indels 116; Gaps 1;

QY 1 MTFDDKMKRPANDEPDQKSCGKRRK-----  
DB 1 MTFDDKMKRPANDEPDQKSCGKRRKGLHLLSPWMPFAATVITLCLVSLTVLQWTLR 60  
QY 25 -----  
DB 61 QVSDLLKQYQANLTQDRIILEGOMLAQKRAENASQESKKELGKIDTLTQKLNKSKRQOE 120

QY 25 -----ESORELKGKIDITTRKLDKSKDEEELLQIONLOALQ 64  
 DB 121 ELIQKONLOALORANSSSEORELKGKIDITTRKLDKSKDEEELLQIONLOALQ 180  
 QY 65 RAANSSSEORELKGKIDITTRKLDKSKDEEELLQIONLOALORANSSGPCPDWL 124  
 DB 181 RAANSSSEORELKGKIDITTRKLDKSKDEEELLQIONLOALORANSSGPCPDWL 240  
 QY 125 WHKENCYLFHGFPGEMKRNQTCOSLGQLOINGADDLFTLQAISHTSPFWIGLHRK 184  
 DB 241 WHKENCYLFHGFPGEMKRNQTCOSLGQLOINGADDLFTLQAISHTSPFWIGLHRK 300  
 QY 185 PGQPMWENGTPLNFOFFKTRGVSLQYSSNCAYLQDGAFAENCILIAFSTCOCKKTNH 244  
 DB 301 PGQPMWENGTPLNFOFFKTRGVSLQYSSNCAYLQDGAFAENCILIAFSTCOCKKTNH 360  
 QY 245 LQI 247  
 DB 361 LQI 363

## RESULT 2

ID 070156 PRELIMINARY: PRT: 364 AA.

AC 070156;  
 DT 01-AUG-1998 (TREMUREL. 07, Created)  
 DT 01-AUG-1998 (TREMUREL. 07, Last sequence update)  
 DT 01-JUN-2001 (TREMUREL. 17, Last annotation update)  
 DE ENDOTHELIAL RECEPTOR FOR OXIDIZED LOW-DENSITY LIPOPROTEIN.  
 GN LOX-1.  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-SHR-SP; TISSUE-KIDNEY.  
 RA MEDLINE=98161826; PubMed=9494115;  
 RX Nagase M., Hirose S., Fujita T.;  
 RT "Unique repetitive sequence and unexpected regulation of expression of rat endothelial receptor for oxidized low-density lipoprotein (LOX-1)."  
 RT Blochem. J. 330:1417-1422(1998).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-SERAGUE-DAMLEY; TISSUE-LIVER;  
 RX MEDLINE=99057940; PubMed=9837956;  
 RA Nagase M., Abe J., Takahashi K., Ando J., Hirose S., Fujita T.;  
 RT "Genomic organization and regulation of expression of the lectin-like oxidized low-density lipoprotein receptor (LOX-1) gene."  
 RT J. Biol. Chem. 273:33702-33707(1998).  
 DR EMBL; AB005900; BAA25785.1; -;  
 DR EMBL; AB018104; BAA35123.1; JOINED.  
 DR EMBL; AB018097; BAA35123.1; JOINED.  
 DR EMBL; AB018098; BAA35123.1; JOINED.  
 DR EMBL; AB018099; BAA35123.1; JOINED.  
 DR EMBL; AB018100; BAA35123.1; JOINED.  
 DR EMBL; AB018101; BAA35123.1; JOINED.  
 DR EMBL; AB018102; BAA35123.1; JOINED.  
 DR EMBL; AB018103; BAA35123.1; JOINED.  
 DR Interpro: IPR001304; lectin\_c.  
 DR Pfam: PF00059; lectin\_c; 1.  
 DR SMART: SM00034; CLECT; 1.  
 DR PROSITE: PS50041; C\_TYPE\_LECTIN\_2; 1.  
 KW Lipoprotein; Receptor; Lectin.  
 SQ SEQUENCE 364 AA; 41890 MW; 0AD2839C07206E09 CRC64;

Query Match 73.7%; Score 972; DB 11; Length 364;  
 Best Local Similarity 53.2%; Pred. No. 4.3e-61;  
 Matches 192; Conservative 22; Mismatches 30; Indels 116; Gaps 2;

DB 1 MAFDKMKPVNGOPDOKSCGKPKGLHLSSSTMCPAAVTLAILCLVSLTVQOTQL 60  
 QY 25 -----ESORELKGKIDITTRKLDKSKDEE 50  
 DB 61 QVSDLLKQYANLTQODHILEGOMSAOKKAEMASOESKRELKEIDITTRKLDKSKDEE 120  
 QY 51 ELIQKONLOALORANSS----- 69  
 DB 121 KLQONONLOALORAVANSEESKWELEKEIDITLMKNGISKDEKELLQONONLOALQ 180  
 QY 70 -----SEORELKGKIDITTRKLDKSKDEEELLQIONLOALORANSSGPCPDWL 124  
 DB 181 KAERYSEORELKEQIDITLSWKLNKSKDEEELLQIONLOALORANSSGPCPDWL 240  
 QY 125 WHKENCYLFHGFPGEMKRNQTCOSLGQLOINGADDLFTLQAISHTSPFWIGLHRK 184  
 DB 241 WHKENCYLFHGFPGEMKRNQTCOSLGQLOINGADDLFTLQAISHTSPFWIGLHRK 300  
 QY 185 PGQPMWENGTPLNFOFFKTRGVSLQYSSNCAYLQDGAFAENCILIAFSTCOCKKTNH 244  
 DB 301 PNHPLWENGSPLSFOFFKTRGVSLQYSSNCAYLQDGAFAENCILIAFSTCOCKKTNH 360  
 QY 245 L 245  
 DB 361 L 361

## RESULT 3

ID 09XTA8 PRELIMINARY: PRT: 278 AA.

AC 09XTA8;  
 DT 01-NOV-1999 (TREMUREL. 12, Created)  
 DT 01-NOV-1999 (TREMUREL. 12, Last sequence update)  
 DT 01-DEC-2001 (TREMUREL. 19, Last annotation update)  
 DE LECTIN-LIKE OXIDIZED LDL RECEPTOR.  
 GN LOX-1.  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 OX NCBI\_TaxID=9986;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Sawamura T., Chen M.;  
 RT "Rabbit lectin-like oxidized LDL receptor 1."  
 RX Submitted (JUL-1998) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AB016237; BAA81912.1; -;  
 DR Interpro: IPR001304; lectin\_c.  
 DR Pfam: PF00059; lectin\_c; 1.  
 DR SMART: SM00034; CLECT; 1.  
 DR PROSITE: PS50041; C\_TYPE\_LECTIN\_2; 1.  
 KW Receptor.  
 SQ SEQUENCE 278 AA; 31646 MW; 25A5E310F823A09B CRC64;

Query Match 48.7%; Score 643; DB 6; Length 278;  
 Best Local Similarity 49.3%; Pred. No. 5.1e-38;  
 Matches 135; Conservative 39; Mismatches 70; Indels 30; Gaps 6;

QY 1 MTFDD-KMKPANDPEPOKSGCKRPKESOREL-----GKIDITTR--- 40  
 DB 5 MAVDDLKVPKPKDOPDOKSGCKRPK-----GLRFLSSPMCPAAVVALGVLCLGSLMTITIMGM 62  
 QY 41 ---RLDESKSDEEELLQIONLOALORANSSSEORELKGKIDITTRKLDKSK 93  
 DB 63 QILOVSDLLKQYANLTQODHILEGOMSAOKKAEMASOESKRELKEIDITTRKLDKSK 122  
 QY 94 EQEELLQKONLOALORANSSGPCPDWLWHKENCYLF-HGPGEMKRNQTCOSLGQ 152  
 DB 123 KOMELNHOYLMQALRKMDNFSGPCPDWLHMGKNKCYLFSSGSEFNNSSOKECLSLDAQ 182  
 QY 153 LLOINGADDLFTLQAISHTSPFWIGLHRKPGQPMWENGTPLNQOFFKTRGVSLQY 212





DT 01-MAY-1997 (TREMBLrel. 03, Created)  
 DT 01-MAY-1997 (TREMBLrel. 03, last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)  
 DE LECTIN-LIKE OXIDIZED LDL RECEPTOR.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;  
 OC Bovidae; Bovinae; Bos.  
 NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=97205278; PubMed=9052782;  
 RA Sawamura T., Kume N., Aoyama T., Moriaki H., Hoshikawa H., Aiba Y.,  
 RA Tanaka T., Miwa S., Katsura Y., Kita T., Masaki T.;  
 RT "An endothelial receptor for oxidized low-density lipoprotein."  
 RL Nature 386:73-77(1997).  
 DR EMBL: D89049; BAA19005.1; -  
 DR HSSP: P20693; 1HLJ; -  
 DR InterPro: IPR001304; lectin\_c.  
 DR Pfam: PF00059; lectin\_c; 1.  
 DR SMART: SM00034; CLECT; 1.  
 DR PROSITE: PS50041; C\_TYPE\_LLECTIN\_2; 1.  
 KW Receptor.  
 SQ SEQUENCE: 270 AA; 30892 MW; 6055B6881AD7053D CRC64;

Query Match 45.2%; Score 596; DB 6; Length 270;  
 Best Local Similarity 44.6%; Pred. No. 1e-34;  
 Matches 125; Conservative 39; Mismatches 70; Indels 46; Gaps 6;

QY 1 MTDDMKRPNDEPKSCGKRR-----ESSQR 29  
 DB 1 MTVDPP-KGKKDDLDGKPNKTAKEVSWRWYPAATLGLVLTLLTLQLSQ- 58  
 QY 30 ELKGKIDITRRKDEKSEELL--OMIQNLGALQRAANFSGPCQDMLHKNCYLF-HGFGMEKNROT 87  
 DB 59 -----VSDLKKQOANTTHOEDILEGOIL-----AORRSKSAOESOKELKEMLETALHK 108  
 QY 88 LNKESKEQELLKQNLQALQRAANFSGPCQDMLHKNCYLF-HGFGMEKNROT 146  
 DB 109 LDRSKKMLHLHONLQVLKEANYSGPCQDMLHKNCYLF-HGFGMEKNROT 168  
 QY 147 QSIAGGLOLQNGADLFTLLQAISSHTSPFWIGLHKKRQGPWLMENGTPLNPFQFTRG 206  
 DB 169 LSLDAHLKLNSTDELEFIQMTAHSFPWMLSMRPNYSWLMEDGTPLNPFQFTRG 228  
 QY 207 VSLQSSNCAYLQDGAFAENCILIAFSICOKKTNHLO 246  
 DB 229 AVSRMYPSCGTCATYQKGTVAENCILIAFSICOKKANLKR 268

RESULT 7  
 ID 09BXN2 PRELIMINARY; PRT; 247 AA.  
 AC 09BXN2;  
 DT 01-JUN-2001 (TREMBLrel. 17, Created)  
 DT 01-JUN-2001 (TREMBLrel. 17, last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, last annotation update)  
 DE DENDRITIC CELL-ASSOCIATED C-TYPE LECTIN-1 (DECTIN-1 RECEPTOR)  
 DE (LECTIN-LIKE RECEPTOR 1) (BETA-GLUCAN RECEPTOR ISOFORM A).  
 GN DECTIN-1 OR DECTIN1 OR BGR.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21363425; PubMed=11470510;  
 RA Yokota K., Takashima A., Bergstresser P.R., Arizumi K.;  
 RT "Identification of a human homologue of the dendritic cell-associated  
 RT C-type lectin-1, dectin-1."  
 RL Gene 272:51-60(2001).  
 RN [2]

RP SEQUENCE FROM N.A.  
 RA Sobanov Y., Bernreiter A., Derdak S., Mechtlcheriakova D., Duechler M.,  
 RA Kalthoff F., Hofer E.;  
 RT "A novel cluster of lectin-like receptor genes expressed in monocytic,  
 RT dendritic and endothelial cells maps close to the NK receptor genes in  
 RT the human NK gene complex."  
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21383615; PubMed=11491532;  
 RA Hernandez-Falcon P., Arce I., Roda-Navarro P., Fernandez-Ruiz E.;  
 RT "Cloning of human DECTIN-1, a novel C-type lectin-like receptor gene  
 RT expressed on dendritic cells."  
 RL Immunogenetics 53:288-295(2001).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RA Hernandez-Falcon P., Arce I., Fernandez-Ruiz E.;  
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-PERIPHERAL BLOOD LEUKOCYTE;  
 RA Willment J.A., Gordon S., Brown G.D.;  
 RT "Characterization of the human beta-glucan receptor and its  
 RT alternatively spliced isoforms."  
 RL J. Biol. Chem. 0:0-0(2001).  
 DR EMBL: AF313468; AAK37473.1; -  
 DR EMBL: AF312373; CAC43847.1; -  
 DR EMBL: AY026769; AAK20114.2; -  
 DR EMBL: AF400595; AAL11711.1; -  
 DR InterPro: IPR002353; Antifreezeit.  
 DR Pfam: PF00059; lectin\_c; 1.  
 DR PRINTS: PR00356; ANTIFREEZEIT.  
 DR SMART: SM00034; CLECT; 1.  
 DR PROSITE: PS50041; C\_TYPE\_LLECTIN\_2; 1.  
 KW Lectin; Receptor.  
 SQ SEQUENCE: 247 AA; 27627 MW; 98393E36976111B9 CRC64;

Query Match 19.6%; Score 258; DB 4; Length 247;  
 Best Local Similarity 31.2%; Pred. No. 6.3e-11;  
 Matches 50; Conservative 41; Mismatches 65; Indels 4; Gaps 3;

QY 86 LKLNESKEQ--ELLQKQNLQALQRAANFSGPCQDMLHKNCYLFHGFG--GMEKN 142  
 DB 85 LSRKKNHSGPTQSLSDSYPTKAVKTGVLSSPCPNMITYEKSCYLSMSLMSWDGS 144  
 QY 143 RQTCQSIGGLOLQNGADLFTLL-QAISHTSPFWIGLHKKRQGPWLMENGTPLNPFQF 201  
 DB 145 KRCQWOLGNSMLKIDSSNELGEFIVKQVSSQPDNSFWIGLSRHPQEVWLMEDGSTFSSNL 204  
 QY 202 KTRGVSLQLYSSNCAYLQDGAFAENCILIAFSICOKK 241  
 DB 205 FQIRTTATQENPSPNCVHWIVYIDQLCSVPSISICEK 244

RESULT 8  
 ID 096PA7 PRELIMINARY; PRT; 168 AA.  
 AC 096PA7;  
 DT 01-DEC-2001 (TREMBLrel. 19, Created)  
 DT 01-DEC-2001 (TREMBLrel. 19, last sequence update)  
 DE BETA-GLUCAN RECEPTOR ISOFORM E.  
 GN BGR.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Willment J.A., Gordon S., Brown G.D.;  
 RT "Characterization of the human beta-glucan receptor and its

RT alternatively spliced isoforms."  
 RL J. Biol. Chem. 0:0(2001).  
 DR EMBL: AF400599; AAL11715.1; -  
 KW Receptor.  
 SQ SEQUENCE 168 AA; 19217 MW; AFD3A86F89BBFFC6 CRC64;

Query Match 19.1%; Score 251.5; DB 4; Length 168;  
 Best Local Similarity 32.6%; Pred. No. 1.2e-10;  
 Matches 47; Conservative 35; Mismatches 59; Indels 3; Gaps 3;

QY 100 QKNOMLGALORANFSGPCPDWLMHKENCYLFHGPF-GWEKNROTCSLGGOLLQING 158  
 DB 23 QSNTRIAVAVSEKV-ISSPCPPNWIYERKCYLFMSLSMDSGSKRQCGQLGSLIKIDS 81  
 QY 159 ADDLFTL-QAISHRTSPFWIGLHKKRQGPWLMENGTPLNQFRTKGVSLQLYSSSNC 217  
 DB 82 SNELEFIVKQVSSQDPNSFVIGLSRQTEVPWLMEDGSTFSSNLFQIRTAQENPSPNC 141  
 QY 218 AYLQGAFAENCILIAFSICOKK 241  
 DB 142 VWIHVSIVYDQCSVPSISICEK 165

RESULT 9  
 Q9HIK3 PRELIMINARY; PRT; 201 AA.  
 ID Q9HIK3  
 AC Q9HIK3:  
 DT 01-MAR-2001 (TREMBLrel. 16, Created)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)  
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)  
 DE PUTATIVE TRANSMEMBRANE PROTEIN DECTIN-1 (DENDRITIC CELL-ASSOCIATED C-  
 DE TYPE LECTIN-1 BETA) (DECTIN-1 RECEPTOR) (LECTIN-LIKE RECEPTOR 1B)  
 DE (BETA-GLUCAN RECEPTOR ISOFORM B).  
 GN DECTIN-1 OR DECTINI OR BGR.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA Grunebach F., Brugger W., Kanz L., Brosart P.;  
 RT "Identification of the human dendritic-cell-associated molecule,  
 RT hdectin-1, by cDNA subtraction and Rapid Amplification of cDNA Ends  
 RT (RACE)."  
 RL Submitted (OCT-2000) to the EMBL/Genbank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Yokota K., Takashima A., Bergstresser P.R., Arizumi K.;  
 RT "Identification of a Human Homolog of the Dendritic Cell-associated C-  
 RT type lectin-1, Dectin-1."  
 RL Submitted (OCT-2000) to the EMBL/Genbank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RA Sobanov V., Bernreiter A., Derdak S., Mechtcheriakova D., Duechler M.,  
 RA Kalthoff F., Hofer E.;  
 RT "A novel cluster of lectin-like receptor genes expressed in monocytic,  
 RT dendritic and endothelial cells maps close to the NK receptor genes in  
 RT the human NK gene complex."  
 RL Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=21383615; PubMed=11491532;  
 RA Hernandez-Falcon P., Arce I., Roda-Navarro P., Fernandez-Ruiz E.;  
 RT "Cloning of human DECTIN-1, a novel C-type lectin-like receptor gene  
 RT expressed on dendritic cells."  
 RL Immunogenetics 53:288-295(2001).  
 RN [5]  
 RP SEQUENCE FROM N.A.  
 RA Hernandez-Falcon P., Arce I., Fernandez-Ruiz E.;  
 RL Submitted (OCT-2001) to the EMBL/Genbank/DBJ databases.  
 RN [6]  
 RP SEQUENCE FROM N.A.

RC TISSUE=PERIPHERAL BLOOD LEUKOCYTE;  
 RA Willment J.A., Gordon S., Brown G.D.;  
 RT "Characterization of the human beta-glucan receptor and its  
 RT alternatively spliced isoforms."  
 RL J. Biol. Chem. 0:0(2001).  
 DR EMBL: AY009090; AAG3923.2; -  
 DR EMBL: AF313469; AAK37474.1; -  
 DR EMBL: AJ312372; CAC43846.1; -  
 DR EMBL: AY026770; AAK20115.1; -  
 DR EMBL: AF400596; AAL11712.1; -  
 DR InterPro: IPR002353; Antifreeze1.  
 DR InterPro: IPR001304; lectin\_c.  
 DR Pfam: PF00059; lectin\_c.1.  
 DR PRINTS: PR00356; ANTIFREEZE1.  
 DR SMART: SM00034; CLECT.1.  
 DR PROSITE: PS50041; C-TYPE-LECTIN\_2; 1.  
 KW Transmembrane; Lectin; Receptor.  
 SQ SEQUENCE 201 AA; 22563 MW; C6ADEE762B2CE968 CRC64;

Query Match 19.0%; Score 251; DB 4; Length 201;  
 Best Local Similarity 35.2%; Pred. No. 1.6e-10;  
 Matches 45; Conservative 32; Mismatches 49; Indels 2; Gaps 2;

QY 116 SGPCPDWLMHKENCYLFHGPF-GWEKNROTCSLGGOLLQINGADLFTL-QAISHRT 173  
 DB 71 SSPPCPNWIYERKCYLFMSLSMDSGSKRQCGQLGSLIKIDSNELEFIVKQVSSQDP 130  
 QY 174 SPFWIGLHKKRQGPWLMENGTPLNQFRTKGVSLQLYSSSNCAYLQGAFAENCILIA 233  
 DB 131 NSWIGLSRQTEVPWLMEDGSTFSSNLFQIRTAQENPSPNCVWIVHSIVYDQCSVP 190  
 QY 234 AFSICOKK 241  
 DB 191 SYSICEK 198

RESULT 10  
 Q9J150 PRELIMINARY; PRT; 244 AA.  
 ID Q9J150  
 AC Q9J150;  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)  
 DE DENDRITIC CELL-ASSOCIATED C-TYPE LECTIN-1.  
 GN CLECSF12 OR DECTIN-1.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=BAB/C;  
 RX MEDLINE=20347934; PubMed=10779524;  
 RA Arizumi K., Shen G.-L., Shikano S., Xu S., Rittner R. III,  
 RA Kumamoto T., Edelbaum D., Morita A., Bergstresser P.R., Takashima A.;  
 RT "Identification of a novel, dendritic cell-associated molecule,  
 RT dectin-1, by subtractive cDNA cloning."  
 RL J. Biol. Chem. 275:20157-20167(2000).  
 DR EMBL: AF262985; AAF72710.1; -  
 DR MGD: MGI:1861431; Clecsf12.  
 DR InterPro: IPR001304; lectin\_c.  
 DR Pfam: PF00059; lectin\_c.1.  
 DR SMART: SM00034; CLECT.1.  
 DR PROSITE: PS50041; C-TYPE-LECTIN\_2; 1.  
 KW Lectin.  
 SQ SEQUENCE 244 AA; 27621 MW; 55A71C04E68CA002 CRC64;

Query Match 17.5%; Score 231; DB 11; Length 244;  
 Best Local Similarity 30.9%; Pred. No. 5e-09;  
 Matches 50; Conservative 27; Mismatches 83; Indels 2; Gaps 2;

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OY 82 DTLTLNLEKSKQOEELLQKNQNLQELQRAANFSGPCPODWLMHKENCYLF-HGPTGWE 140
DB 82 DNLSRNKEHKKPTSSSIDKVAAPSKQTTGFSQSLPNTIMHGKSCYLFSGSGMSWY 141
OY 141 KNRQTOOSLGGLLOINGADLTFTI-LOAISHTSPFWIGLHKRPQOPLMENGPTLNF 199
DB 142 GSRKHSQDLAHLKTKINDNSPEFTESQTSRSHINAFWIGLSRQSGPWFMEGSAFPP 201
OY 200 QEFKTRGVSLQLYSSNCAYLQDGAFAENCILIAFSICOK 241
DB 202 NSFQVRNTVPQESLHNCAWIMHSEVYNQICMSSYSICKE 243

RESULT 11
O95L6 PRELIMINARY; PRT; 381 AA.
AC 095L6;
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DE DENDRITIC CELL-SPECIFIC ICAM-3 GRABBING NONINTEGRIN.
OC Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OC NCBI_TaxID=9544;
RN 11
RX MEDLINE=21465051; PubMed=11581396;
RA Barilaud F., Pohlmann S., Sparwasser T., Kimata M.T., Choi Y.K.,
RA Haggerty B.S., Ahmad N., Macfarlan T., Edwards T.G., Leslie G.J.,
RA Arnason J., Reinhart T.A., Kimata J.T., Littman D.R., Hoxie J.A.,
RA Doms R.W.;
RT "Functional and antigenic characterization of human, rhesus macaque,
RT pigtailed macaque, and murine dc-sign.";
RL J. Virol. 75:10281-10289(2001).
DR EMBL: AF369755; AAL14438.1; -.
KW Integrin.
SQ SEQUENCE 381 AA; 42897 MW; 01FE7B0B42C91D49 CRC64;

Query Match 17.0%; Score 224.5; DB 6; Length 381;
Best Local Similarity 25.8%; Pred. No. 2.3e-08;
Matches 74; Conservative 50; Mismatches 98; Indels 65; Gaps 13;

OY 6 KMRPANDPPOKS-----CGKRPRESOREL-----KGK 34
DB 83 QLKVAVSELSKSKQOEIYQELTRLKAAGVGLPEKSKQOEIYQELTRLKAAGVGLPEKSK 142
OY 35 IDTI-----TR-----KLDEKSKQOEELQMLQALQRAANFSGPCPODWLMHKENCYLFHG 79
DB 143 LQEIYQELTRLKAAGVGLPEKSK-QOEIYQELSLKAAGVGLPEKSKQOEIYQELTRLKA 201
OY 80 KIDTLTLKLNKESKEOE---ELLQKNQNLQELQRAANFSGPCPODWLMHKENCYLFHG 135
DB 202 AVGLP-----DRSKQOEIYQELIQ---LKAVERLCR---PCWEMTFEGNGCYFMSNS 250
OY 136 PFEWKNRQTCQSLGGLLOINGADLTFTIQAISHTSPFWIGLHKRPQOPLMENGPT 195
DB 251 QRNMHNSITACQEVGAQLVYIKSAEQNFLOQSSRSNRFYTWGLSLDNLHGCTQWVDGS 310
OY 196 PL--NPOEFKTRGVSLQLYSSNCAYLQDGAFAENCILIAFSICOK 240
DB 311 PLPSFKQYWNKGEPNNV-GEEDCAEFSGNGMNDKCNLAKFWICK 356

RESULT 12
O95L6 PRELIMINARY; PRT; 381 AA.
AC 095L6;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)

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DE DENDRITIC CELL-SPECIFIC ICAM-3 GRABBING NONINTEGRIN.
OS Macaca nemestrina (Pig-tailed macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OC NCBI_TaxID=9545;
RN 11
RX MEDLINE=21465051; PubMed=11581396;
RA Barilaud F., Pohlmann S., Sparwasser T., Kimata M.T., Choi Y.K.,
RA Haggerty B.S., Ahmad N., Macfarlan T., Edwards T.G., Leslie G.J.,
RA Arnason J., Reinhart T.A., Kimata J.T., Littman D.R., Hoxie J.A.,
RA Doms R.W.;
RT "Functional and antigenic characterization of human, rhesus macaque,
RT pigtailed macaque, and murine dc-sign.";
RL J. Virol. 75:10281-10289(2001).
DR EMBL: AF343727; AAL14428.1; -.
KW Integrin.
SQ SEQUENCE 381 AA; 42951 MW; C4F6E23D454B74A CRC64;

Query Match 16.9%; Score 223.5; DB 6; Length 381;
Best Local Similarity 25.8%; Pred. No. 2.7e-08;
Matches 74; Conservative 51; Mismatches 97; Indels 65; Gaps 13;

OY 6 KMRPANDPPOKS-----CGKRPRESOREL-----KGK 34
DB 83 QLKVAVSELSKSKQOEIYQELTRLKAAGVGLPEKSKQOEIYQELTRLKAAGVGLPEKSK 142
OY 35 IDTI-----TR-----KLDEKSKQOEELQMLQALQRAANFSGPCPODWLMHKENCYLFHG 79
DB 143 LQEIYQELTRLKAAGVGLPEKSK-QOEIYQELSLKAAGVGLPEKSKQOEIYQELTRLKA 201
OY 80 KIDTLTLKLNKESKEOE---ELLQKNQNLQELQRAANFSGPCPODWLMHKENCYLFHG 135
DB 202 AVGLP-----DRSKQOEIYQELIQ---LKAVERLCR---PCWEMTFEGNGCYFMSNS 250
OY 136 PFEWKNRQTCQSLGGLLOINGADLTFTIQAISHTSPFWIGLHKRPQOPLMENGPT 195
DB 251 QRNMHNSITACQEVGAQLVYIKSAEQNFLOQSSRSNRFYTWGLSLDNLHGCTQWVDGS 310
OY 196 PL--NPOEFKTRGVSLQLYSSNCAYLQDGAFAENCILIAFSICOK 240
DB 311 PLPSFKQYWNKGEPNNV-GEEDCAEFSGNGMNDKCNLAKFWICK 356

RESULT 13
O96Q04 PRELIMINARY; PRT; 360 AA.
AC 096Q04;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE SPC-SIGNIA TYPE II ISOFORM.
GN CD209.
OS Homo sapiens (human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OC NCBI_TaxID=9606;
RN 11
RX MEDLINE=11337487;
RA Mummidi S., Catano G., Lam L., Hoefle A., Telles V., Begum K.,
RA Jimenez F., Ahuja S.S., Ahuja S.K.;
RT "Extensive repertoire of Membrane-bound and soluble Dendritic Cell-
RT specific ICAM-3-grabbing Nonintegrin 1 (DC-SIGN1) and DC-SIGN2
RT isoforms. Inter-Individual Variation In Expression Of DC-SIGN
RT Isoforms. Transcripts.";
RL J. Biol. Chem. 276:33196-33212(2001).
DR EMBL: AY042226; AAK91851.1; -.
SQ SEQUENCE 360 AA; 41009 MW; 6ABE2B9A9AEDFAA8 CRC64;

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Query Match 16.9%; Score 223; DB 4; Length 360;  
Best Local Similarity 26.0%; Pred. No. 2.8e-08;  
Matches 67; Conservative 54; Mismatches 107; Indels 30; Gaps 10;

```
OY 6 KMKPANDPEPOKS-----CGKKPKESORELKIGDITD---TRKIDESK 47
   :| | | | |
Db 85 RLKAAGVGLPEKSKLOEYQELTWLKAAGVGLPEKSKMOEYQELTRLKAAGVGLPEKSK 144
   :| | | | |
OY 48 EOELLQMIQLOEALORANSSESQ--RELKGIIDLTLKLNKSKOEELLQKNQNL 105
   :| | | | |
Db 145 -QOEYQELTRLKAAGVGLPEKSKQOEYQELT-RLKAAGVGLPEKSK-QOEYQELTQL 201
   :| | | | |
OY 106 QEALORANFSGPCPODMLMKENCY-LFHGPFGEKNRQTCOSLGQLQINGADLTF 164
   :| | | | |
Db 202 KAAVERLCH---PCPWEWTFPGNCYFMSNSQRNMHDSITACKEGVQOLVYIKSAEQNF 258
   :| | | | |
OY 165 ILQAISSHTTSPWIGLHRRKKGQPLWENGTP--NFOFKTRGVSLQYSSNCAYLQD 222
   :| | | | |
Db 259 LQLOSSRSNRFTWMLGSLDNOEGTWQWDGSPLLPFSKQYNNRGPNNV-GEEDCAEFSG 317
   :| | | | |
OY 223 GAVFAENCILIAFSTICK 240
   :| | | | |
Db 318 NGWMDKCNLAKFWICK 335
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## RESULT 14

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096005 PRELIMINARY; PRT; 380 AA.
AC 096005;
ID 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE SDC-SIGNIA TYPE I ISOFORM.
CN C2209.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=11337487;
RA Mummidi S., Catano G., Lam L., Hoeffle A., Telles V., Begum K.,
RA Jimenez F., Ahuja S.S., Ahuja S.K.;
RT "Extensive Repertoire of Membrane-bound and Soluble Dendritic Cell-
RT specific ICAM-3-grabbing Nonintegrin 1 (DC-SIGN1) and DC-SIGN2
RT Isoforms. Inter-individual Variation in Expression of DC-SIGN
RT Transcripts.";
RT J. Biol. Chem. 276:33196-33212(2001).
DR EMBL; AY042225; AAK91850.1;
SQ SEQUENCE 380 AA; 43330 MW; BCF9CC45ABEF6B02 CRC64;
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Query Match 16.9%; Score 223; DB 4; Length 380;  
Best Local Similarity 26.0%; Pred. No. 3e-08;  
Matches 67; Conservative 54; Mismatches 107; Indels 30; Gaps 10;

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OY 6 KMKPANDPEPOKS-----CGKKPKESORELKIGDITD---TRKIDESK 47
   :| | | | |
Db 105 RLKAAGVGLPEKSKLOEYQELTWLKAAGVGLPEKSKMOEYQELTRLKAAGVGLPEKSK 164
   :| | | | |
OY 48 EOELLQMIQLOEALORANSSESQ--RELKGIIDLTLKLNKSKOEELLQKNQNL 105
   :| | | | |
Db 165 -QOEYQELTRLKAAGVGLPEKSKQOEYQELT-RLKAAGVGLPEKSK-QOEYQELTQL 221
   :| | | | |
OY 106 QEALORANFSGPCPODMLMKENCY-LFHGPFGEKNRQTCOSLGQLQINGADLTF 164
   :| | | | |
Db 222 KAAVERLCH---PCPWEWTFPGNCYFMSNSQRNMHDSITACKEGVQOLVYIKSAEQNF 278
   :| | | | |
OY 165 ILQAISSHTTSPWIGLHRRKKGQPLWENGTP--NFOFKTRGVSLQYSSNCAYLQD 222
   :| | | | |
Db 279 LQLOSSRSNRFTWMLGSLDNOEGTWQWDGSPLLPFSKQYNNRGPNNV-GEEDCAEFSG 337
   :| | | | |
OY 223 GAVFAENCILIAFSTICK 240
   :| | | | |
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Db 338 NGWMDKCNLAKFWICK 355

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RESULT 15
096000 PRELIMINARY; PRT; 380 AA.
AC 096000;
ID 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE SDC-SIGNIB TYPE I ISOFORM.
CN C2209.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxId=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX PubMed=11337487;
RA Mummidi S., Catano G., Lam L., Hoeffle A., Telles V., Begum K.,
RA Jimenez F., Ahuja S.S., Ahuja S.K.;
RT "Extensive Repertoire of Membrane-bound and Soluble Dendritic Cell-
RT specific ICAM-3-grabbing Nonintegrin 1 (DC-SIGN1) and DC-SIGN2
RT Isoforms. Inter-individual Variation in Expression of DC-SIGN
RT Transcripts.";
RT J. Biol. Chem. 276:33196-33212(2001).
DR EMBL; AY042230; AAK91851.1;
SQ SEQUENCE 380 AA; 43125 MW; F3D098F9FB7D044B CRC64;
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Query Match 16.9%; Score 223; DB 4; Length 380;  
Best Local Similarity 26.0%; Pred. No. 3e-08;  
Matches 67; Conservative 54; Mismatches 107; Indels 30; Gaps 10;

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Db 105 RLKAAGVGLPEKSKLOEYQELTWLKAAGVGLPEKSKMOEYQELTRLKAAGVGLPEKSK 164
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OY 48 EOELLQMIQLOEALORANSSESQ--RELKGIIDLTLKLNKSKOEELLQKNQNL 105
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OY 106 QEALORANFSGPCPODMLMKENCY-LFHGPFGEKNRQTCOSLGQLQINGADLTF 164
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Db 222 KAAVERLCH---PCPWEWTFPGNCYFMSNSQRNMHDSITACKEGVQOLVYIKSAEQNF 278
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Db 279 LQLOSSRSNRFTWMLGSLDNOEGTWQWDGSPLLPFSKQYNNRGPNNV-GEEDCAEFSG 337
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OY 223 GAVFAENCILIAFSTICK 240
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Db 338 NGWMDKCNLAKFWICK 355
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